



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 197717

TO: Juliet Switzer  
Location: REM-2A61/2C70  
Art Unit: 1634  
Friday, August 18, 2006  
Case Serial Number: 10/600642

From: Barb O'Bryen  
Location: Biotech-Chem Library  
Remsen 1a69  
Phone: 571-272-2518

*BOB*  
barbara.obryen@uspto.gov

### Search Notes

Juliet,

For the S/L search:

no suitable hits in EST for either sequence

on disc	{	N-GeneSeq =	ngs1.res	, ngs2.res
		Issued-Patents-NA	iss1.res	iss2.res
		Genbank/EMBL	ge1.res	ge2.res
		Published-Applications-NA-Main	pubmain1.res	pubmain2.res
		Published-Applications-NA-New	pubnew1.res	pubnew2.res

Also included are the results tables for the standard searches of Segs 1, 2, 5, 6, & 10.

Barb

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:39:06 ; Search time 217.292 Seconds  
(without alignments)  
5591.547 Million cell updates/sec

Title: US-10-600-642A-5

Perfect score: 19  
Sequence: 1 ccattctcttgaaatctc 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_env: \*  
2: gb\_pat: \*  
3: gb\_ph: \*  
4: gb\_pl: \*  
5: gb\_pr: \*  
6: gb\_ro: \*  
7: gb\_sts: \*  
8: gb\_sy: \*  
9: gb\_un: \*  
10: gb\_vi: \*  
11: gb\_ov: \*  
12: gb\_hcg: \*  
13: gb\_in: \*  
14: gb\_om: \*  
15: gb\_ba: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	2 E54415	E54415 Specific an
2	19	100.0	19	2 AR408842	AR408842 Sequence
3	19	100.0	442	2 E54412	E54412 Specific an
4	19	100.0	442	2 AR408839	AR408839 Sequence
5	19	100.0	442	15 AB022064	AB022064 Pectinatu
6	19	100.0	624	2 E54411	E54411 Specific an
7	19	100.0	624	2 AR408838	AR408838 Sequence
8	19	100.0	624	15 AB022063	AB022063 Pectinatu
9	18	94.7	110000	15 AE016879_25	Continuation (26 o
10	18	94.7	110000	15 AE016879_26	Continuation (27 o
11	18	94.7	110000	15 AE017225_26	Continuation (27 o
12	18	94.7	110000	15 AE017334_25	Continuation (26 o
13	18	94.7	110000	15 AE017334_26	Continuation (27 o
14	18	94.7	110000	15 AE017355_26	Continuation (27 o
15	18	94.7	110000	15 CP000001_26	Continuation (27 o
16	17.4	91.6	1297	2 CQ979403	CQ979403 Sequence
17	17.4	91.6	1371	2 CQ979407	CQ979407 Sequence
18	17.4	91.6	2520	4 AB012628	AB012628 Adiantum

100%  
100%

C 19	17.4	91.6	4557	4	AB012631	AB012631 Adiantum
C 20	17.4	91.6	68480	5	AC026426	AC026426 Homo sapi
C 21	17.4	91.6	110000	4	AP008214_126	Continuation (127
C 22	17.4	91.6	146969	5	AC092945	AC092945 Homo sapi
C 23	17.4	91.6	152702	4	AP005162	AP005162 Oryza sat
C 24	17.4	91.6	161353	12	AC174462	AC174462 Bos tauru
C 25	17.4	91.6	178320	4	AY360391	AY360391 Oryza sat
C 26	17.4	91.6	184235	4	AP005166	AP005166 Oryza sat
C 27	17.4	91.6	186747	6	AC155266	AC155266 Mus muscu
C 28	17.4	91.6	187972	4	AY360390	AY360390 Oryza sat
C 29	17.4	91.6	195998	12	AC128308	AC128308 Rattus no
C 30	17.4	91.6	220797	12	AC153718	AC153718 Bos tauru
C 31	17.4	91.6	227769	12	AC112437	AC112437 Rattus no
C 32	17.4	91.6	232415	12	AC099429	AC099429 Rattus no
C 33	17.4	91.6	245663	12	AC096102	AC096102 Rattus no
C 34	17.4	91.6	246011	6	AL929585	AL929585 Mouse DNA
C 35	17.4	91.6	252991	12	AC172968	AC172968 Bos tauru
C 36	17	89.5	509	2	CQ476058	CQ476058 Sequence
C 37	17	89.5	563	2	CQ506009	CQ506009 Sequence
C 38	17	89.5	581	7	BV268474	BV268474 S235P6405
C 39	17	89.5	2027	2	CQ493216	CQ493216 Sequence
C 40	17	89.5	4221	2	BD171173	BD171173 Novel gen
C 41	17	89.5	4221	2	BD183502	BD183502 Novel gen
C 42	17	89.5	4221	5	AB051524	AB051524 Homo sapi
C 43	17	89.5	4258	5	AK096603	AK096603 Homo sapi
C 44	17	89.5	4341	5	BC037300	BC037300 Homo sapi
C 45	17	89.5	63987	12	AC080154	AC080154 Homo sapi

# ALIGNMENTS

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:30:09 ; Search time 27.4613 Seconds  
(without alignments)  
4823.973 Million cell updates/sec

Title: US-10-600-642A-5

Perfect score: 19  
Sequence: 1 ccatctcttgaaatctc 19

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_8.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	3	AAZ91775 Spacer re
2	19	100.0	19	4	AAI71859 Pectinatu
3	19	100.0	19	14	Adw11499 PCR prime
4	19	100.0	442	3	AAZ91772 Spacer re
5	19	100.0	442	4	AAI71856 Pectinatu
6	19	100.0	624	3	AAZ91771 Spacer re
7	19	100.0	624	4	AAI71855 Pectinatu
8	17.4	91.6	1297	14	Adw38752 Pectinatu
9	17.4	91.6	1371	14	Adw38756 Pectinatu
10	17.4	91.6	46675	11	ACN44684 Mouse gen
11	17	89.5	485	4	AAI02322 Human rep
12	17	89.5	485	4	ABA07627 Human ova
13	17	89.5	509	5	ABV07934 Human pro
14	17	89.5	563	5	ABV37857 Human pro
15	17	89.5	1607	5	ABA21307 Human ner
16	17	89.5	2000	11	ACL38212 Rice stre
17	17	89.5	2000	12	Adj41083 Plant cDN
18	17	89.5	2027	5	ABV25094 Human pro

mut  
prim

19	17	89.5	3101	10	ADC30468	Adc30468 Human nov
20	17	89.5	3861	5	ABA21308	AbA21308 Human ner
21	17	89.5	4221	6	ABN83982	Abn83982 Human gen
22	16.4	86.3	479	11	ADT96902	Adt96902 Colon can
23	16.4	86.3	479	11	ADK43384	Adk43384 Human cDN
24	16.4	86.3	766	6	ABN99167	Abn99167 Arabidops
25	16.4	86.3	1696	6	ABZ70806	Abz70806 Human rib
C 26	16.4	86.3	5175	13	ADS17665	AdS17665 Human pol
C 27	16.4	86.3	5211	13	ADS17714	AdS17714 Cysteine
C 28	16.4	86.3	5463	13	ADS17718	AdS17718 GAL4 pept
C 29	16.4	86.3	5489	14	ADW92027	Adw92027 DNA seque
C 30	16.4	86.3	5490	3	AAZ45690	Aaz45690 cDNA sequ
C 31	16.4	86.3	5490	4	AAC92076	Aac92076 Human min
C 32	16.4	86.3	5490	10	ADB46005	Adb46005 Human min
C 33	16.4	86.3	5490	14	ADW86203	Adw86203 Human VPA
C 34	16.4	86.3	5565	13	ADS17726	AdS17726 MS2 pepti
C 35	16.4	86.3	5889	13	ADS17722	AdS17722 Green flu
C 36	16.4	86.3	6825	13	ADS17732	AdS17732 Luciferas
C 37	16.4	86.3	7302	5	AAS87290	Aas87290 DNA encod
C 38	16.4	86.3	32183	4	AAI99267	Aai99267 Human exc
C 39	16.4	86.3	32183	5	AAI63617	Aai63617 Human kid
C 40	16.4	86.3	32192	4	AAI99266	Aai99266 Human exc
C 41	16.4	86.3	32192	5	AAI63616	Aai63616 Human kid
C 42	16	84.2	1470	5	AAS75618	Aas75618 DNA encod
C 43	16	84.2	2212	4	AAK52374	Aak52374 Human pol
C 44	16	84.2	2226	4	AAC85790	Aac85790 hMEn1 cDN
C 45	16	84.2	2226	8	ABX96871	Abx96871 DNA encod

## ALIGNMENTS

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:57:34 ; Search time 8.03911 Seconds  
(without alignments)  
4422.263 Million cell updates/sec

Title: US-10-600-642A-5

Perfect score: 19

Sequence: 1 ccattcttgaataatctc 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/ina/ECTUS\_COMB.seq:\*
- 8: /EMC Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*
- 9: /EMC Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*
- 10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	19	100.0	19	3	US-09-762-633-5 Sequence 5, Appli
2	19	100.0	442	3	US-09-762-633-2 Sequence 2, Appli
3	19	100.0	624	3	US-09-762-633-1 Sequence 1, Appli
4	16.4	86.3	5490	3	US-09-607-510-1 Sequence 1, Appli
5	16	84.2	2226	3	US-10-117-846-5 Sequence 5, Appli
6	16	84.2	2754	5	US-10-470-554-1 Sequence 1, Appli
7	16	84.2	2754	5	US-10-470-554-3 Sequence 3, Appli
8	16	84.2	3148	3	US-10-117-846-7 Sequence 7, Appli
9	15.8	83.2	305	3	US-09-513-999C-2094 Sequence 2094, Ap
10	15.8	83.2	638	3	US-09-533-559-6274 Sequence 6274, Ap
11	15.8	83.2	2289	3	US-08-948-705-8 Sequence 8, Appli
12	15.8	83.2	2289	3	US-09-510-543-8 Sequence 8, Appli
13	15.8	83.2	2289	4	US-09-502-945-8 Sequence 8, Appli
14	15.8	83.2	2409	3	US-09-510-543-9 Sequence 9, Appli
15	15.8	83.2	41743	3	US-09-949-016-13796 Sequence 13796, A
16	15.4	81.1	213	3	US-09-583-110-107 Sequence 107, App
17	15.4	81.1	540	3	US-09-248-796A-12682 Sequence 12682, A
18	15.4	81.1	5558	3	US-08-961-527-103 Sequence 103, App
19	15.4	81.1	9511	2	US-07-925-695-6 Sequence 6, Appli
20	15.4	81.1	9511	2	US-07-925-695-7 Sequence 7, Appli
21	15.4	81.1	45716	3	US-08-965-048-5 Sequence 5, Appli
22	15.4	81.1	45989	3	US-08-965-048-6 Sequence 6, Appli
23	15.4	81.1	72600	4	US-09-531-120-206 Sequence 206, App

#### ALIGNMENTS

c	24	15.4	81.1	283538	3	US-09-949-016-13506	Sequence 13506, A
c	25	15	78.9	6676	3	US-09-949-016-16533	Sequence 16533, A
c	26	15	78.9	13906	3	US-09-949-016-14730	Sequence 14730, A
c	27	14.8	77.9	32	3	US-09-826-509-400	Sequence 400, App
c	28	14.8	77.9	32	3	US-09-826-509-401	Sequence 401, App
c	29	14.8	77.9	107	3	US-09-959-716-23	Sequence 23, Appl
c	30	14.8	77.9	255	3	US-09-134-000C-511	Sequence 511, App
c	31	14.8	77.9	304	3	US-09-389-681-301	Sequence 301, App
c	32	14.8	77.9	304	3	US-09-620-405B-301	Sequence 301, App
c	33	14.8	77.9	304	3	US-09-339-338-301	Sequence 301, App
c	34	14.8	77.9	304	3	US-09-433-826B-301	Sequence 301, App
c	35	14.8	77.9	304	3	US-09-604-287A-301	Sequence 301, App
c	36	14.8	77.9	304	3	US-09-834-759-301	Sequence 301, App
c	37	14.8	77.9	304	3	US-09-590-751A-301	Sequence 301, App
c	38	14.8	77.9	304	3	US-09-551-621-301	Sequence 301, App
c	39	14.8	77.9	304	3	US-09-551-621A-301	Sequence 301, App
c	40	14.8	77.9	304	3	US-10-076-622-301	Sequence 301, App
c	41	14.8	77.9	304	4	US-10-124-805-301	Sequence 301, App
c	42	14.8	77.9	347	3	US-08-956-171B-1159	Sequence 1159, Ap
c	43	14.8	77.9	347	3	US-08-781-986A-1159	Sequence 1159, Ap
c	44	14.8	77.9	367	3	US-09-621-976-1116	Sequence 1116, Ap
c	45	14.8	77.9	413	3	US-09-513-999C-4023	Sequence 4023, Ap

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 06:08:00 ; Search time 95.3716 Seconds  
(without alignments)  
2447.953 Million cell updates/sec

Title: US-10-600-642A-5

Perfect score: 19

Sequence: 1 ccatctcttgaataatctc 19

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 1892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	8	US-10-600-642-5
C 2	19	100.0	442	8	US-10-600-642-2
C 3	19	100.0	624	8	US-10-600-642-1
C 4	17.4	91.6	578	4	US-09-925-065A-503267
C 5	17.4	91.6	578	4	US-09-925-065A-503268
C 6	17.4	91.6	578	4	US-09-925-065A-503269
C 7	17.4	91.6	578	5	US-09-925-065A-503267
C 8	17.4	91.6	578	5	US-09-925-065A-503268
C 9	17.4	91.6	578	5	US-09-925-065A-503269
C 10	17.4	91.6	1297	9	US-10-862-063A-20
C 11	17.4	91.6	1371	9	US-10-862-063A-24
C 12	17.4	91.6	3750	8	US-10-437-963-50726
C 13	17.4	91.6	4734	8	US-10-437-963-50775
C 14	17.4	91.6	46675	6	US-10-087-192-1255
15	17	89.5	485	3	US-09-764-891-2323
16	17	89.5	485	6	US-10-205-428-184
C 17	17	89.5	509	9	US-10-357-930-7925

C	18	17	89.5	563	9	US-10-357-930-37876	Sequence 37876, A
	19	17	89.5	2000	8	US-10-260-238-2083	Sequence 2083, Ap
	20	17	89.5	2027	9	US-10-357-930-25083	Sequence 25083, A
C	21	17	89.5	2253	8	US-10-437-963-56352	Sequence 56352, A
C	22	16.4	86.3	467	16	US-11-087-099-174	Sequence 174, App
C	23	16.4	86.3	479	6	US-10-066-543-2421	Sequence 2421, Ap
C	24	16.4	86.3	636	4	US-09-925-065A-471436	Sequence 471436, A
C	25	16.4	86.3	636	5	US-09-925-065A-471436	Sequence 471436, A
C	26	16.4	86.3	661	4	US-09-925-065A-874526	Sequence 874526, A
C	27	16.4	86.3	661	5	US-09-925-065A-874526	Sequence 874526, A
C	28	16.4	86.3	766	3	US-09-770-445-935	Sequence 935, App
C	29	16.4	86.3	2871	8	US-10-437-963-27977	Sequence 27977, A
C	30	16.4	86.3	4347	8	US-10-437-963-50702	Sequence 50702, A
C	31	16.4	86.3	4710	8	US-10-437-963-50734	Sequence 50734, A
C	32	16.4	86.3	5490	6	US-10-163-587A-16	Sequence 16, Appl
C	33	16.4	86.3	5490	10	US-10-898-653-6	Sequence 6, Appl
C	34	16.4	86.3	7302	10	US-10-450-763-23094	Sequence 23094, A
C	35	16.4	86.3	32183	7	US-10-242-355-1031	Sequence 1031, Ap
C	36	16.4	86.3	32192	7	US-10-242-355-1030	Sequence 1030, Ap
C	37	16.4	86.3	87384	9	US-10-719-993-6781	Sequence 6781, Ap
	38	16	84.2	50	16	US-11-175-859-70793	Sequence 70793, A
	39	16	84.2	508	4	US-09-925-065A-789633	Sequence 789633, A
	40	16	84.2	508	5	US-09-925-065A-789633	Sequence 789633, A
C	41	16	84.2	1470	10	US-10-450-763-11422	Sequence 11422, A
C	42	16	84.2	2226	6	US-10-117-846-5	Sequence 5, Appl
C	43	16	84.2	2340	8	US-10-276-774-955	Sequence 955, App
C	44	16	84.2	2754	8	US-10-470-554-1	Sequence 1, Appl
C	45	16	84.2	2754	8	US-10-470-554-3	Sequence 3, Appl

# ALIGNMENTS

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 06:09:34 ; Search time 10.2347 Seconds  
(without alignments)  
2967.635 Million cell updates/sec

Title: US-10-600-642A-5

Perfect score: 19

Sequence: 1 ccatctcttgaataatctc 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.New.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	89.5	631	8	US-11-266-748A-360975 Sequence 360975,
C 2	17	89.5	631	8	US-11-266-748A-444354 Sequence 444354,
C 3	16.4	86.3	411	8	US-11-266-748A-421952 Sequence 421952,
4	16.4	86.3	485	8	US-11-266-748A-11619 Sequence 11619, A
C 5	16.4	86.3	485	8	US-11-266-748A-64384 Sequence 64384, A
6	16.4	86.3	485	8	US-11-266-748A-67216 Sequence 67216, A
7	16.4	86.3	941	8	US-11-266-748A-188139 Sequence 188139,
C 8	16.4	86.3	941	8	US-11-266-748A-242236 Sequence 242236,
C 9	16.4	86.3	2130	8	US-11-266-748A-74318 Sequence 74318, A
C 10	16.4	86.3	2130	8	US-11-266-748A-127129 Sequence 127129,
C 11	16.4	86.3	5175	6	US-10-547-530-4 Sequence 4, Appl
C 12	16.4	86.3	5211	6	US-10-547-530-53 Sequence 53, Appl
C 13	16.4	86.3	5463	6	US-10-547-530-57 Sequence 57, Appl
C 14	16.4	86.3	5565	6	US-10-547-530-65 Sequence 65, Appl
C 15	16.4	86.3	5889	6	US-10-547-530-61 Sequence 61, Appl
C 16	16.4	86.3	6825	6	US-10-547-530-71 Sequence 71, Appl
C 17	16.4	86.3	40173	8	US-11-266-748A-29048 Sequence 29048, A
C 18	16	84.2	939	8	US-11-266-748A-171169 Sequence 171169,
C 19	16	84.2	1358	8	US-11-266-748A-256796 Sequence 256796,
C 20	16	84.2	1358	8	US-11-266-748A-317313 Sequence 317313,
C 21	16	84.2	1370	8	US-11-266-748A-171170 Sequence 171170,
C 22	16	84.2	1373	8	US-11-266-748A-4178 Sequence 4178, Ap
C 23	16	84.2	2231	8	US-11-266-748A-78060 Sequence 78060, A

#### ALIGNMENTS

24	16	84.2	2231	8	US-11-266-748A-130871	Sequence 130871,
C 25	16	84.2	2958	8	US-11-266-748A-27310	Sequence 27310, A
C 26	16	84.2	3400	8	US-11-266-748A-30321	Sequence 30321, A
27	15.8	83.2	25	9	US-11-348-413-677830	Sequence 677830,
28	15.8	83.2	25	9	US-11-348-413-677831	Sequence 677831,
29	15.8	83.2	302	9	US-11-348-413-2016	Sequence 2016, Ap
30	15.8	83.2	848	8	US-11-266-748A-178638	Sequence 178638,
C 31	15.8	83.2	1968	9	US-11-218-305-18096	Sequence 18096, A
C 32	15.8	83.2	39638	8	US-11-266-748A-23809	Sequence 23809, A
33	15.8	83.2	128361	6	US-10-505-928-151	Sequence 151, App
C 34	15.8	83.2	1421559	8	US-11-266-748A-28208	Sequence 28208, A
35	15.4	81.1	304	8	US-11-266-748A-166770	Sequence 166770,
36	15.4	81.1	473	8	US-11-266-748A-300328	Sequence 300328,
C 37	15.4	81.1	990	9	US-11-348-413-634	Sequence 634, App
C 38	15.4	81.1	1245	8	US-11-266-748A-185143	Sequence 185143,
C 39	15.4	81.1	1245	8	US-11-266-748A-192633	Sequence 192633,
40	15.4	81.1	1245	8	US-11-266-748A-240771	Sequence 240771,
C 41	15.4	81.1	1251	9	US-11-056-355B-90108	Sequence 90108, A
C 42	15.4	81.1	1251	9	US-11-056-355B-93864	Sequence 93864, A
43	15.4	81.1	1658	8	US-11-266-748A-185142	Sequence 185142,
C 44	15.4	81.1	1658	8	US-11-266-748A-240770	Sequence 240770,
C 45	15.4	81.1	2043	6	US-10-953-349-25266	Sequence 25266, A

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:46:51 / Search time 218.255 Seconds  
(without alignments)  
4868.007 Million cell updates/sec

Title: US-10-600-642a-5

Perfect score: 19

Sequence: 1 ccatcctctgaataatc 19

Scoring table: IDENTITY\_NUC

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:\*  
1: gb\_esc1:\*  
2: gb\_esc3:\*  
3: gb\_esc4:\*  
4: gb\_esc5:\*  
5: gb\_esc6:\*  
6: gb\_esc7:\*  
7: gb\_esc8:\*  
8: gb\_esc9:\*  
9: gb\_esc10:\*  
10: gb\_esc11:\*  
11: gb\_esc12:\*  
12: gb\_esc13:\*  
13: gb\_esc14:\*  
14: gb\_esc15:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	921	7	BE965735
2	18	94.7	724	9	DN879125
3	17.4	91.6	115	11	AY203370
4	17.4	91.6	276	7	BB295113
5	17.4	91.6	394	5	CJ282616
6	17.4	91.6	430	12	BZ779062
7	17.4	91.6	445	11	AO617138
8	17.4	91.6	482	7	BE353220
9	17.4	91.6	527	12	CB447341
10	17.4	91.6	548	2	BI423416
11	17.4	91.6	589	8	CV524665
12	17.4	91.6	613	2	BJ188256
13	17.4	91.6	628	10	DT595457
14	17.4	91.6	629	1	AL703784
15	17.4	91.6	644	11	BH015400
16	17.4	91.6	645	7	AW931562
17	17.4	91.6	684	7	AW218125
18	17.4	91.6	746	8	CV502261
19	17.4	91.6	748	9	CX759904

20	17.4	91.6	783	14	BX968075	BX968075 Forward s
21	17.4	91.6	802	3	BQ506745	BQ506745 EST614160
22	17.4	91.6	813	10	DT582372	DT582372 BHE01-5ms
23	17.4	91.6	848	14	CT138335	CT138335 Sus scrofa
24	17.4	91.6	867	14	AG837463	AG837463 Oryza sat
25	17.4	91.6	878	5	CK248403	CK248403 EST732040
26	17.4	91.6	914	14	DU948828	DU948828 399018 To
27	17.4	91.6	2244	13	CL946607	CL946607 OEIFS005
28	17	89.5	355	1	AA446265	AA446265 zme0h11.8
29	17	89.5	383	10	T26578	T26578 AB325A1R In
30	17	89.5	458	11	AQ701345	AQ701345 HS_2133_A
31	17	89.5	473	1	AL135682	AL135682 DKFZp7620
32	17	89.5	502	9	DA146221	DA146221 DA146221
33	17	89.5	505	11	AZ430402	AZ430402 LM0214D20
34	17	89.5	527	9	DA175599	DA175599 DA175599
35	17	89.5	549	9	DA552897	DA552897 DA552897
36	17	89.5	551	14	CT048243	CT048243 Sus scrofa
37	17	89.5	555	9	DB005316	DB005316 DB005316
38	17	89.5	560	9	DB108010	DB108010 DB108010
39	17	89.5	569	9	DA875421	DA875421 DA875421
40	17	89.5	571	9	DA157867	DA157867 DA157867
41	17	89.5	574	9	DA133385	DA133385 DA133385
42	17	89.5	575	9	DA354964	DA354964 DA354964
43	17	89.5	575	9	DA765933	DA765933 DA765933
44	17	89.5	579	9	DA091280	DA091280 DA091280
45	17	89.5	590	9	DA283653	DA283653 DA283653

#### ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:39:06 ; Search time 228.729 Seconds  
(without alignments)  
5591.547 Million cell updates/sec

Title: US-10-600-642A-6

Perfect score: 19.6

Sequence: 1 tctcytctcacaagtgtgsc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_env:\*
- 2: gb\_pat:\*
- 3: gb\_ph:\*
- 4: gb\_pl:\*
- 5: gb\_pr:\*
- 6: gb\_ro:\*
- 7: gb\_sts:\*
- 8: gb\_sy:\*
- 9: gb\_un:\*
- 10: gb\_vi:\*
- 11: gb\_ov:\*
- 12: gb\_htg:\*
- 13: gb\_in:\*
- 14: gb\_om:\*
- 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.6	100.0	442	2 E54412	E54412 Specific an
C 2	19.6	100.0	442	2 AR408839	AR408839 Sequence
C 3	19.6	100.0	442	15 AB022064	AB022064 Pectinatu
C 4	19.6	100.0	624	2 E54411	E54411 Specific an
C 5	19.6	100.0	624	2 AR408838	AR408838 Sequence
C 6	19.6	100.0	624	15 AB022063	AB022063 Pectinatu
7	19.6	100.0	160383	6 AC163994	AC163994 Mus muscu
8	19.6	100.0	171181	6 AC101796	AC101796 Mus muscu
9	18.4	93.9	20	2 E54416	E54416 Specific an
10	18.4	93.9	20	2 AR408843	AR408843 Sequence
11	18	91.8	59805	12 AC101664	AC101664 Mus muscu
C 12	18	91.8	190750	6 AC116322	AC116322 Mus muscu
C 13	18	91.8	216807	12 AC174477	AC174477 Mus muscu
C 14	17.6	89.8	110000	4 AP008208	Continuation (7 of
C 15	17.6	89.8	110000	12 AC171053_0	AC171053 Bos tauru
C 16	17.6	89.8	110000	12 AC171053_1	Continuation (2 of
C 17	17.6	89.8	150597	12 AP005005	AP005005 Oryza sat
18	17.6	89.8	156603	4 AP004752	AP004752 Oryza sat

C	19	17.6	89.8	220110	12	AC162023	AC162023 Bos tauru
C	20	17	86.7	816	7	BV647532	BV647532 S215P6174
C	21	17	86.7	964	6	GPAS36353	AJ536353 Graphiuru
C	22	17	86.7	966	6	GLO536356	AJ536356 Graphiuru
C	23	17	86.7	4197	5	HSM803592	AL832285 Homo sapi
C	24	17	86.7	7096	5	AB061835	AB061835 Homo sapi
C	25	17	86.7	62001	12	AC015206	AC015206 Drosophila
C	26	17	86.7	79622	12	AC036119	AC036119 Homo sapi
C	27	17	86.7	90050	12	AC172645	AC172645 Bos tauru
C	28	17	86.7	110000	4	AP007159_15	Continuation (16 of
C	29	17	86.7	110000	12	AC171343_2	Continuation (3 of
C	30	17	86.7	110724	5	AC099063	AC099063 Homo sapi
C	31	17	86.7	115681	12	AC158694	AC158694 Bos tauru
C	32	17	86.7	121023	14	DQ020489	DQ020489 Sus scrofa
C	33	17	86.7	126281	5	HS223B1	AL031943 Human DNA
C	34	17	86.7	133195	11	AL935052	AL935052 Zebrafish
C	35	17	86.7	134210	5	AC005052	AC005052 Homo sapi
C	36	17	86.7	138641	5	AL513348	AL513348 Human DNA
C	37	17	86.7	143251	11	BX510924	BX510924 Zebrafish
C	38	17	86.7	151959	12	AC021689	AC021689 Homo sapi
C	39	17	86.7	153072	12	CT573036	CT573036 Mus muscu
C	40	17	86.7	154948	12	AC141985	AC141985 Rattus no
C	41	17	86.7	156127	12	AC160233	AC160233 Rhinoloph
C	42	17	86.7	159561	12	AC159955	AC159955 Rhinoloph
C	43	17	86.7	159981	5	AC016817	AC016817 Homo sapi
C	44	17	86.7	166176	12	AC104143	AC104143 Drosophila
C	45	17	86.7	167336	12	AC021350	AC021350 Homo sapi

ALIGNMENTS



GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:30:09 ; Search time 28.9067 Seconds  
(without alignments)  
4823.973 Million cell updates/sec

Title: US-10-600-642A-6

Perfect score: 19.6

Sequence: 1 tctctctcacaaagtgttggc 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.6	100.0	442	3 AAZ91772	Aaz91772 Spacer re
C 2	19.6	100.0	442	4 AAI71856	Aai71856 Pectinatu
C 3	19.6	100.0	624	3 AAZ91771	Aaz91771 Spacer re
C 4	19.6	100.0	624	4 AAI71855	Aai71855 Pectinatu
5	18.4	93.9	20	3 AAZ91776	Aaz91776 Spacer re
6	18.4	93.9	20	4 AAI71860	Aai71860 Pectinatu
C 7	17	86.7	2126	10 ADC30432	Adc30432 Human nov
C 8	16.8	85.7	520	10 ADB56829	Adb56829 Toxicity-
C 9	16.8	85.7	520	13 ADV40260	Adv40260 Rat cardi
C 10	16.6	84.7	42104	11 ACN44606	Acn44606 Human gen
11	16.4	83.7	665	10 ADC77280	Adc77280 DNA homol
12	16.4	83.7	665	10 ADK57163	Adk57163 Plant DNA
13	16.4	83.7	665	10 ADK57378	Adk57378 Plant DNA
14	16.4	83.7	665	10 ADK59919	Adk59919 Plant DNA
15	16.4	83.7	667	10 ADC76706	Adc76706 DNA homol
16	16.4	83.7	1672	13 ADX60600	Adx60600 Plant ful
17	16.4	83.7	2000	6 ABZ15692	Abz15692 Arabidops
C 18	16.4	83.7	92099	14 ADZ12547	Adz12547 Murine ca

19	16.4	83.7	178825	11	ACN45144	Acn45144 Mouse gen
C 20	16.4	83.7	188267	14	ADZ13837	Adz13837 Human can
C 21	16.4	83.7	188794	12	ADQ59476	Adq59476 Human can
C 22	16	81.6	258	6	ABN76996	Abn76996 Human nuc
C 23	16	81.6	408	12	ADJ83967	Adj83967 Human asp
C 24	16	81.6	414	12	ADJ83963	Adj83963 Human asp
C 25	16	81.6	427	3	AAC27951	Aac27951 Human sec
C 26	16	81.6	465	12	ADJ83971	Adj83971 Human asp
C 27	16	81.6	516	12	ADJ83969	Adj83969 Human asp
C 28	16	81.6	547	6	ABQ55556	Abq55556 Human ova
C 29	16	81.6	777	12	ADJ83961	Adj83961 Human asp
C 30	16	81.6	952	6	ABL55149	AbL55149 Human cyt
C 31	16	81.6	1029	12	ADJ83962	Adj83962 Human asp
C 32	16	81.6	1450	10	ADC30297	Adc30297 Human nov
C 33	16	81.6	1695	10	ADJ46102	Adj46102 Human epi
C 34	16	81.6	2168	10	ADA53116	Ada53116 Human cod
C 35	16	81.6	2334	2	AAV18481	Aav18481 Human zin
36	16	81.6	2561	2	AAV29269	Aav29269 Nucleotid
37	16	81.6	2561	6	ABT11028	Abt11028 Human bre
38	16	81.6	2561	7	AD873151	Ad873151 Human kid
39	16	81.6	2561	7	ADM42005	Adm42005 cDNA elev
40	16	81.6	2561	15	AEF74641	Aef74641 Human pol
41	16	81.6	2738	2	AAZ33549	Aaz33549 Human bre
42	16	81.6	2790	2	AAV18480	Aav18480 BOP1 cDNA
43	16	81.6	2828	6	ABN86525	Abn86525 Nucleotid
44	16	81.6	2828	12	ADQ95837	Adq95837 T cell ac
45	16	81.6	3975	6	ABN86526	Abn86526 Nucleotid

ALIGNMENTS

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:57:34 ; Search time 8.46222 Seconds  
(without alignments)  
4422.263 Million cell updates/sec

Title: US-10-600-642A-6

Perfect score: 19.6

Sequence: 1 tctctctcacaagtgtgsc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.6	100.0	442	3	US-09-762-633-2 Sequence 2, Appli
C 2	19.6	100.0	624	3	US-09-762-633-1 Sequence 1, Appli
C 3	18.4	93.9	20	3	US-09-762-633-6 Sequence 6, Appli
C 4	17	86.7	9110	3	US-09-949-016-13642 Sequence 13642, A
C 5	16.4	83.7	601	3	US-09-949-016-88998 Sequence 88998, A
C 6	16.4	83.7	601	3	US-09-949-016-88999 Sequence 88999, A
C 7	16.4	83.7	162465	3	US-09-949-016-14264 Sequence 14264, A
C 8	16	81.6	427	3	US-09-513-999C-32026 Sequence 32026, A
C 9	16	81.6	2168	4	US-10-094-749-684 Sequence 684, App
C 10	16	81.6	2539	3	US-09-949-016-5569 Sequence 5569, Ap
C 11	16	81.6	2790	2	US-08-718-661-1 Sequence 1, Appli
C 12	16	81.6	5385	3	US-09-920-804-1 Sequence 1, Appli
C 13	16	81.6	28585	3	US-09-949-016-17311 Sequence 17311, A
C 14	15.6	79.6	5621	3	US-09-566-921-106 Sequence 106, App
C 15	15.4	78.6	347	3	US-09-513-999C-31944 Sequence 31944, A
C 16	15.4	78.6	386	3	US-09-621-976-8578 Sequence 8578, Ap
C 17	15.4	78.6	541	3	US-09-621-976-15802 Sequence 15802, A
C 18	15.4	78.6	566	3	US-09-621-976-3389 Sequence 3389, Ap
C 19	15.4	78.6	601	3	US-09-949-016-44283 Sequence 44283, A
C 20	15.4	78.6	601	3	US-09-949-016-65452 Sequence 65452, A
C 21	15.4	78.6	601	3	US-09-949-016-146866 Sequence 146866, A
C 22	15.4	78.6	601	3	US-09-949-016-146867 Sequence 146867, A
C 23	15.4	78.6	601	3	US-09-949-016-146868 Sequence 146868, A

Sequence 1497, Ap  
Sequence 6009, Ap  
Sequence 8, Appli  
Sequence 15864, A  
Sequence 15123, A  
Sequence 17338, A  
Sequence 17339, A  
Sequence 14144, A  
Sequence 14145, A  
Sequence 13655, A  
Sequence 17235, A  
Sequence 13002, A  
Sequence 9401, Ap  
Sequence 95, Appli  
Sequence 1, Appli  
Sequence 12386, A  
Sequence 16915, A  
Sequence 11579, A  
Sequence 11581, A  
Sequence 2033, Ap  
Sequence 8345, Ap

US-09-248-796A-1497  
US-09-533-559-6009  
US-09-724-864-8  
US-09-949-016-15864  
US-09-949-016-15123  
US-09-949-016-17338  
US-09-949-016-17339  
US-09-949-016-14144  
US-09-949-016-14145  
US-09-949-016-13655  
US-09-949-016-17235  
US-09-949-016-13002  
US-09-313-294A-7401  
US-09-566-921-95  
US-09-051-019-1  
US-09-949-016-12386  
US-09-949-016-16915  
US-09-949-016-11579  
US-09-396-196G-11581  
US-09-396-196G-11581  
US-09-297-648-2033  
US-09-270-767-8345

#### ALIGNMENTS

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 06:08:00 ; Search time 100.391 Seconds  
 (without alignments)  
 2447.953 Million cell updates/sec

Title: US-10-600-642A-6  
 Perfect score: 19.6  
 Sequence: 1 tctcytcacaaagtgtggc 20

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications NA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19.6	100.0	442	8	US-10-600-642-2
C 2	19.6	100.0	624	8	US-10-600-642-1
C 3	18.4	93.9	20	8	US-10-600-642-6
4	18	91.8	976	8	US-10-424-599-52516
5	18	91.8	1037	16	US-11-096-568A-7060
6	17	86.7	371	8	US-10-767-701-19326
C 7	17	86.7	376	8	US-10-424-599-130958
8	16.6	84.7	485	4	US-09-925-065A-635628
9	16.6	84.7	485	4	US-09-925-065A-635629
10	16.6	84.7	485	5	US-09-925-065A-635628
11	16.6	84.7	485	5	US-09-925-065A-635629
12	16.6	84.7	547	4	US-09-925-065A-635630
13	16.6	84.7	547	5	US-09-925-065A-635630
14	16.6	84.7	550	4	US-09-925-065A-634326
15	16.6	84.7	550	5	US-09-925-065A-634326
C 16	16.6	84.7	42104	6	US-10-087-192-1138
C 17	16.4	83.7	488	8	US-10-424-599-110087

C 18	16.4	83.7	539	6	US-10-027-632-140171	Sequence 140171,
C 19	16.4	83.7	539	7	US-10-027-632-140171	Sequence 140171,
C 20	16.4	83.7	608	12	US-10-301-480-44785	Sequence 44785, A
21	16.4	83.7	608	12	US-10-301-480-658194	Sequence 658194,
C 22	16.4	83.7	615	4	US-09-925-065A-638398	Sequence 638398,
C 23	16.4	83.7	615	5	US-09-925-065A-638398	Sequence 638398,
C 24	16.4	83.7	618	4	US-09-925-065A-524353	Sequence 524353,
C 25	16.4	83.7	618	5	US-09-925-065A-524353	Sequence 524353,
C 26	16.4	83.7	622	6	US-10-027-632-185639	Sequence 185639,
C 27	16.4	83.7	622	7	US-10-027-632-185639	Sequence 185639,
C 28	16.4	83.7	665	10	US-10-487-901-4546	Sequence 4546, Ap
29	16.4	83.7	665	10	US-10-487-901-4761	Sequence 4761, Ap
30	16.4	83.7	665	10	US-10-487-901-7302	Sequence 7302, Ap
31	16.4	83.7	806	12	US-10-301-480-597879	Sequence 597879,
32	16.4	83.7	806	12	US-10-301-480-1211288	Sequence 1211288,
33	16.4	83.7	966	4	US-09-925-065A-547753	Sequence 547753,
34	16.4	83.7	966	4	US-09-925-065A-547754	Sequence 547754,
35	16.4	83.7	966	4	US-09-925-065A-547755	Sequence 547755,
36	16.4	83.7	966	5	US-09-925-065A-547753	Sequence 547753,
37	16.4	83.7	966	5	US-09-925-065A-547754	Sequence 547754,
38	16.4	83.7	966	5	US-09-925-065A-547755	Sequence 547755,
39	16.4	83.7	966	12	US-10-301-480-525703	Sequence 525703,
40	16.4	83.7	966	12	US-10-301-480-525704	Sequence 525704,
41	16.4	83.7	966	12	US-10-301-480-525705	Sequence 525705,
42	16.4	83.7	966	12	US-10-301-480-1139112	Sequence 1139112,
43	16.4	83.7	966	12	US-10-301-480-1139113	Sequence 1139113,
44	16.4	83.7	966	12	US-10-301-480-1139114	Sequence 1139114,
45	16.4	83.7	1672	8	US-10-425-114-31443	Sequence 31443, A

## ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 06:09:34 ; Search time 10.7733 Seconds  
(without alignments)  
2967.635 Million cell updates/sec

Title: US-10-600-642A-6

Perfect score: 19.6

Sequence: 1 tctcyctcacaagtgtgac 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_NA\_New.\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	91.8	1027	9	US-11-056-355B-54899	Sequence 54899, A
2	16.6	84.7	4337	8	US-11-266-748A-28282	Sequence 28282, A
3	16.4	83.7	853	8	US-11-266-748A-39712	Sequence 39712, A
4	16.4	83.7	2921	9	US-11-218-305-13146	Sequence 13146, A
C 5	16.4	83.7	162354	8	US-11-266-748A-23437	Sequence 23437, A
C 6	16	81.6	1000	8	US-11-266-748A-404777	Sequence 404777, A
7	16	81.6	1000	8	US-11-266-748A-475823	Sequence 475823, A
C 8	16	81.6	1242	8	US-11-266-748A-26781	Sequence 26781, A
C 9	16	81.6	1566	8	US-11-217-529-79698	Sequence 79698, A
C 10	16	81.6	1695	6	US-10-508-063A-2	Sequence 2, Appli
11	16	81.6	4074	8	US-11-217-529-4467	Sequence 4467, App
12	16	81.6	88607	6	US-10-540-898-625	Sequence 625, App
C 13	16	81.6	185035	8	US-11-266-748A-59932	Sequence 59932, A
14	15.8	80.6	1929	6	US-10-449-902-6866	Sequence 6866, AP
15	15.8	80.6	1942	6	US-10-449-902-27655	Sequence 27655, A
C 16	15.6	79.6	418	8	US-11-266-748A-119678	Sequence 119678, A
C 17	15.6	79.6	465	8	US-11-266-748A-87744	Sequence 87744, A
18	15.6	79.6	465	8	US-11-266-748A-140555	Sequence 140555, A
19	15.6	79.6	515	8	US-11-266-748A-49163	Sequence 49163, A
20	15.6	79.6	1215	9	US-11-056-355B-58762	Sequence 58762, A
C 21	15.6	79.6	1520	8	US-11-266-748A-188237	Sequence 188237, A
22	15.6	79.6	1520	8	US-11-266-748A-242281	Sequence 242281, A
23	15.4	78.6	427	8	US-11-266-748A-50420	Sequence 50420, A

#### ALIGNMENTS

24	15.4	78.6	427	8	US-11-266-748A-207588	Sequence 207588, A
C 25	15.4	78.6	427	8	US-11-266-748A-233135	Sequence 233135, A
26	15.4	78.6	695	8	US-11-266-748A-266635	Sequence 266635, A
C 27	15.4	78.6	695	8	US-11-266-748A-327152	Sequence 327152, A
28	15.4	78.6	1057	8	US-11-216-545-1067	Sequence 1067, AP
C 29	15.4	78.6	1361	6	US-10-449-902-26437	Sequence 26437, A
30	15.4	78.6	2052	8	US-11-217-529-634	Sequence 634, App
C 31	15.4	78.6	2723	9	US-11-218-305-1630	Sequence 1630, App
32	15.4	78.6	390183	6	US-10-540-898-937	Sequence 937, App
33	15.4	78.6	634888	6	US-10-533-365-1	Sequence 1, Appli
C 34	15.2	77.6	1616	6	US-10-953-349-23939	Sequence 23939, A
C 35	15.2	77.6	1616	9	US-11-056-355B-54014	Sequence 54014, A
C 36	15.2	77.6	1859	8	US-11-216-545-4999	Sequence 4999, AP
C 37	15.2	77.6	2011	8	US-11-216-545-5000	Sequence 5000, AP
38	15.2	77.6	3203	8	US-11-266-748A-352168	Sequence 352168, A
C 39	15.2	77.6	3203	8	US-11-266-748A-435547	Sequence 435547, A
C 40	15.2	77.6	7758	6	US-10-505-928-236	Sequence 236, App
C 41	15.2	77.6	7762	8	US-11-266-748A-32565	Sequence 32565, A
C 42	15.2	77.6	100167	8	US-11-266-748A-61848	Sequence 61848, A
C 43	15	76.5	380	8	US-11-266-748A-374961	Sequence 374961, A
C 44	15	76.5	380	8	US-11-266-748A-458340	Sequence 458340, A
C 45	15	76.5	461	8	US-11-266-748A-91384	Sequence 91384, A

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:46:51 ; Search time 229.742 Seconds  
(without alignments)  
4868.007 Million cell updates/sec

Title: US-10-600-642A-6

Perfect score: 19.6

Sequence: 1 tctcytcacaaagtttggc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_estc.\*  
7: gb\_est2.\*  
8: gb\_est7.\*  
9: gb\_est8.\*  
10: gb\_est9.\*  
11: gb\_gss1.\*  
12: gb\_gss2.\*  
13: gb\_gss3.\*  
14: gb\_gss4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.6	100.0	833	14	CR004625
2	18	91.8	440	3	BQ489531
3	18	91.8	772	9	CX547812
4	18	91.8	807	9	CX702729
5	18	91.8	949	3	BU855413
6	17.6	89.8	525	11	AQ775512
7	17.6	89.8	693	14	CR842343
8	17	86.7	509	7	AW755115
9	17	86.7	510	9	DB322477
10	17	86.7	584	13	CW147321
11	17	86.7	616	13	CW147322
12	17	86.7	635	8	CO998387
13	17	86.7	658	10	DR683655
14	17	86.7	664	8	CX064606
15	17	86.7	667	12	BZ883851
16	17	86.7	671	4	CB002007
17	17	86.7	676	4	CB004765
18	17	86.7	686	3	BM764933
19	17	86.7	700	3	BM763755

C	20	17	86.7	705	4	BX451773
C	21	17	86.7	736	3	BQ635125
C	22	17	86.7	736	14	CT073182
C	23	17	86.7	738	10	DR693743
C	24	17	86.7	756	5	CF662726
C	25	17	86.7	768	11	BZ168835
C	26	17	86.7	821	5	CK686238
C	27	17	86.7	830	13	DU319612
C	28	17	86.7	846	9	DR020109
C	29	17	86.7	853	13	DU403127
C	30	17	86.7	855	10	DR687891
C	31	17	86.7	896	5	CK208620
C	32	17	86.7	902	14	DU889130
C	33	17	86.7	907	10	DT489827
C	34	17	86.7	937	4	BX435916
C	35	17	86.7	960	13	DU054235
C	36	17	86.7	960	13	DU094768
C	37	17	86.7	1108	5	CK209285
C	38	17	86.7	1121	5	CK208604
C	39	17	86.7	1228	12	BZ691139
C	40	17	86.7	1428	6	CR625387
C	41	16.8	85.7	520	1	AI103854
C	42	16.6	84.7	169	12	CC378107
C	43	16.6	84.7	280	2	BI032935
C	44	16.6	84.7	425	12	BZ941497
C	45	16.6	84.7	668	14	DU486105

#### ALIGNMENTS

BX451773	BX451773
BQ635125	NXR07077_C
CT073182	Sub sciof
DR693743	EST108383
CF662726	CLX04a14
BZ168835	CH230-414
CK686238	ZF101-P00
DU319612	109844802
DR020109	STRS1_34
DU403127	109844827
DR687891	EST107797
CK208620	FGAS02033
DU889130	387123 To
DT489827	WS02543.B
BX435916	BX435916
DU054235	144670 To
DU094768	109848 To
CK209285	FGAS02104
CK208604	FGAS02031
BZ691139	SP_Ba000
CR625387	full_leng
AI103854	EST213143
CC378107	PUBG48TB
BI032935	MR4-NN020
BZ941497	CH240-92G
DU486105	109842109

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:39:06 ; Search time 228.729 Seconds  
(without alignments)  
5591.547 Million cell updates/sec

Title: US-10-600-642A-10

Perfect score: 20  
Sequence: 1 cgtatccagatggatatt 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
C 1	20	100.0	20	2	AR034877 Sequence
2	20	100.0	20	2	AR034887 Sequence
3	20	100.0	20	2	E54420 Specific an
4	20	100.0	20	2	E54421 Specific an
5	20	100.0	20	2	AR408847 Sequence
6	20	100.0	1033	1	AF530356 Unculture
7	20	100.0	1328	1	AY916235 Unculture
8	20	100.0	1328	1	AY975925 Unculture
9	20	100.0	1328	1	AY976361 Unculture
10	20	100.0	1328	1	AY980600 Unculture
11	20	100.0	1328	1	AY981083 Unculture
12	20	100.0	1328	1	AY982219 Unculture
13	20	100.0	1328	1	AY982353 Unculture
14	20	100.0	1367	15	AY428574 Pectinatu
15	20	100.0	1449	1	AF132277 Unculture
16	20	100.0	1498	15	AF373027 Pectinatu
17	20	100.0	1515	1	DQ237944 Unculture
18	19	95.0	1412	15	AB052711 Acetobact

19	19	95.0	1414	15	AB052710	Acetobact
20	19	95.0	1492	1	AF349415	Unculture
21	19	95.0	1493	1	AF349422	Unculture
C 22	19	95.0	157430	6	AC135378	Mus muscu
23	19	95.0	184556	6	AC117230	Mus muscu
24	18.4	92.0	426	1	AY846114	Unculture
25	18.4	92.0	893	1	DQ263519	Unculture
26	18.4	92.0	173853	6	AC154726	Mus muscu
C 27	18.4	92.0	176213	6	CT030645	Mouse DNA
28	18	90.0	1409	15	AF127400	Glucunace
29	18	90.0	69947	5	AL512285	Human DNA
C 30	18	90.0	71561	12	AL928982_6	Continuation (7 of
31	18	90.0	107335	5	HS145B12_5	Human DNA
C 32	18	90.0	124283	12	AC108368	AC108368 Pan trogl
C 33	18	90.0	152320	5	AC084377	AC084377 Homo sapi
C 34	18	90.0	182035	12	AC068040	AC068040 Homo sapi
35	18	90.0	203185	6	AC120132	AC120132 Mus muscu
36	18	90.0	225692	12	AC165112	AC165112 Bos tauru
37	18	90.0	301967	12	AC172248	AC172248 Bos tauru
38	17.4	87.0	241	15	AY072698	AY072698 Glucunace
C 39	17.4	87.0	270	15	AF440747	AF440747 Asaia sp.
40	17.4	87.0	322	15	AY669514	AY669514 Acetobact
41	17.4	87.0	403	1	AY683282	AY683282 Unculture
42	17.4	87.0	403	1	AY683287	AY683287 Unculture
43	17.4	87.0	819	15	ASP012542	AJ012542 Acetobact
44	17.4	87.0	1004	15	AY360335	AY360335 Asaia sia
45	17.4	87.0	1137	1	AY678229	AY678229 Unculture

ALIGNMENTS

100%  
100%

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:30:09 ; Search time 28.9067 Seconds  
(without alignments)  
4823.973 Million cell updates/sec

Title: US-10-600-642A-10

Perfect score: 20

Sequence: 1 cgtatccagatggatatt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 524920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_8.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	20	2	Aat69583 Pectinatu
2	20	100.0	20	3	Aaz91781 PCR prime
3	20	100.0	20	3	Aaz91780 PCR prime
4	20	100.0	20	4	Aai71864 Pectinatu
5	20	100.0	20	4	Aai71865 Pectinatu
6	20	100.0	20	4	Adw11498 PCR prime
7	17	85.0	110000	11	Acn44932 Mouse gen
8	17	85.0	110000	11	Acn44932_1
9	16.8	84.0	20	2	Aat69579 Pectinatu
10	16.8	84.0	20	14	Adw11505 PCR prime
11	16.4	82.0	128963	12	Adq97110 Human can
12	16	80.0	251	8	Abx38205 Bovine ES
13	16	80.0	652	11	ACL32681 Rice abio
14	15	80.0	948	12	Ado30434 Mouse GPC
15	15.8	79.0	552	12	Adl03813 DNA encod
16	15.8	79.0	588	12	Ach72375 Human gen
17	15.8	79.0	682	4	AAS43271 DNA encod
18	15.8	79.0	682	4	AAS43346 DNA encod

C 19	15.8	79.0	682	4	AAI85744	AAI85744 Human pol
C 20	15.8	79.0	716	3	AAF12014	AAF12014 Aspergill
C 21	15.8	79.0	716	13	ADU56055	ADU56055 Aspergill
C 22	15.8	79.0	716	14	ADZ94058	ADZ94058 Aspergill
C 23	15.8	79.0	805	8	ABZ52207	ABZ52207 Aspergill
C 24	15.8	79.0	1128	8	ACA24573	ACA24573 Prokaryot
C 25	15.8	79.0	1167	13	ADT47769	ADT47769 Bacterial
C 26	15.8	79.0	1359	8	ACA29316	ACA29316 Prokaryot
C 27	15.8	79.0	1435	13	ADX65584	ADX65584 Plant ful
C 28	15.8	79.0	1470	10	ADF01029	ADF01029 Bacterial
C 29	15.8	79.0	1506	11	ACH99697	ACH99697 Klebsiell
C 30	15.8	79.0	9630	14	AEA61219	AEA61219 Human GPX
C 31	15.8	79.0	9866	4	AAK73616	AAK73616 Human imm
C 32	15.8	79.0	12384	8	AAD48288	AAD48288 Human glu
C 33	15.8	79.0	56743	4	AAK68202	AAK68202 Human imm
C 34	15.8	79.0	56743	4	AAK81760	AAK81760 Human imm
C 35	15.8	79.0	62909	4	AAF28545	AAF28545 Genomic f
C 36	15.8	79.0	110000	14	AEA61169_1	Continuation (2 of
C 37	15.8	79.0	127917	13	ADR52731_1	ADR52731 Drug ther
C 38	15.8	79.0	133462	13	ABD32622	ABD32622 Mouse can
C 39	15.4	77.0	35	9	AAI57313	AAI57313 rRNA-spec
C 40	15.4	77.0	100	8	ACD70504	ACD70504 E. coli K
C 41	15.4	77.0	222	9	ADA29686	ADA29686 DNA encod
C 42	15.4	77.0	384	2	AAT05157	AAT05157 Dermatoph
C 43	15.4	77.0	447	11	ACH96211	ACH96211 Klebsiell
C 44	15.4	77.0	449	5	AAS90102	AAS90102 DNA encod
C 45	15.4	77.0	1186	13	ADX59778	ADX59778 Plant ful

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:57:34 ; Search time 8.46222 Seconds  
(without alignments)  
4422.263 Million cell updates/sec

Title: US-10-600-642A-10

Perfect score: 20

Sequence: 1 cgtatccagatggatatt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCrUS COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	20	2	US-08-875-445-8 Sequence 8, Appli
C 2	20	100.0	20	2	US-08-875-445-18 Sequence 18, Appl
C 3	20	100.0	20	3	US-09-762-633-10 Sequence 10, Appl
C 4	16.8	84.0	20	2	US-08-875-445-4 Sequence 4, Appli
C 5	16.8	84.0	20	2	US-08-875-445-14 Sequence 14, Appl
C 6	16.8	84.0	20	3	US-09-762-633-11 Sequence 11, Appl
C 7	16	80.0	601	3	US-09-949-016-130489 Sequence 130489,
C 8	16	80.0	197875	3	US-09-949-016-15425 Sequence 15425, A
C 9	15.8	79.0	552	3	US-09-540-236-1499 Sequence 1499, Ap
C 10	15.8	79.0	601	3	US-09-949-016-17718 Sequence 17718, A
C 11	15.8	79.0	601	3	US-09-949-016-151695 Sequence 151695,
C 12	15.8	79.0	601	3	US-09-949-016-151696 Sequence 151696,
C 13	15.8	79.0	601	3	US-09-949-016-170323 Sequence 170323,
C 14	15.8	79.0	601	3	US-09-949-016-180600 Sequence 180600,
C 15	15.8	79.0	716	3	US-09-533-559-4537 Sequence 4537, Ap
C 16	15.8	79.0	1470	3	US-09-543-681A-1314 Sequence 1314, Ap
C 17	15.8	79.0	1506	3	US-09-489-039A-5492 Sequence 5492, Ap
C 18	15.8	79.0	12385	3	US-09-822-862-3 Sequence 3, Appli
C 19	15.8	79.0	46288	3	US-09-949-016-14999 Sequence 14999, A
C 20	15.8	79.0	46311	3	US-09-949-016-15000 Sequence 15000, A
C 21	15.8	79.0	62909	3	US-09-596-002-32 Sequence 32, Appl
C 22	15.8	79.0	87617	3	US-09-949-016-16551 Sequence 16551, A
C 23	15.8	79.0	88002	3	US-09-949-002-639 Sequence 639, App

24	15.8	79.0	88002	3	US-09-949-002-717 Sequence 717, App
C 25	15.8	79.0	92334	3	US-09-949-016-13920 Sequence 13920, A
C 26	15.8	79.0	92363	3	US-09-949-016-12146 Sequence 12146, A
C 27	15.8	79.0	98567	3	US-09-949-016-11750 Sequence 11750, A
28	15.8	79.0	100567	3	US-09-949-016-16934 Sequence 16934, A
29	15.8	79.0	28338	3	US-09-949-016-13506 Sequence 13506, A
30	15.8	79.0	31766	3	US-09-949-016-16001 Sequence 16001, A
31	15.4	77.0	222	3	US-09-328-352-973 Sequence 973, App
C 32	15.4	77.0	447	3	US-09-489-039A-2006 Sequence 2006, Ap
C 33	15.4	77.0	601	3	US-09-949-016-139703 Sequence 139703,
C 34	15.4	77.0	601	3	US-09-949-016-139704 Sequence 139704,
35	15.4	77.0	3012	2	US-07-991-867B-21 Sequence 21, Appl
36	15.4	77.0	3012	2	US-08-107-755A-21 Sequence 21, Appl
37	15.4	77.0	3012	2	US-08-544-332-21 Sequence 21, Appl
38	15.4	77.0	3012	3	US-09-370-861A-21 Sequence 21, Appl
39	15.4	77.0	3907	2	US-07-991-867B-33 Sequence 33, Appl
40	15.4	77.0	3907	2	US-08-107-755A-33 Sequence 33, Appl
41	15.4	77.0	3907	2	US-08-544-332-33 Sequence 33, Appl
42	15.4	77.0	3907	3	US-09-370-861A-33 Sequence 33, Appl
43	15.4	77.0	6768	2	US-08-107-755A-1 Sequence 1, Appli
44	15.4	77.0	7445	3	US-09-178-973B-8 Sequence 8, Appli
45	15.4	77.0	7445	3	US-09-419-568F-8 Sequence 8, Appli

#### ALIGNMENTS



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Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: August 17, 2006, 06:08:00 ; Search time 100.391 Seconds  
(without alignments)  
2447.953 Million cell updates/sec

Title: US-10-600-642A-10  
Perfect score: 20  
Sequence: 1 cgtatccagatgatatt 20

Scoring table: IDENTITY\_NUC ,  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	8	US-10-600-642-10
C 2	17	85.0	1157	8	US-10-437-963-24506
C 3	17	85.0	374849	6	US-10-087-192-1627
4	16.8	84.0	20	8	US-10-600-642-11
5	16.4	82.0	1385	10	US-10-750-185-25980
6	16.4	82.0	1385	10	US-10-750-623-25980
7	16.4	82.0	4584	8	US-10-437-963-88605
C 8	16.4	82.0	21322	9	US-10-741-600-17860
C 9	16.4	82.0	21322	10	US-10-995-561-13418
10	16.4	82.0	128963	11	US-10-330-773-86
C 11	16.4	82.0	199130	9	US-10-741-600-17617
C 12	16.4	82.0	199130	10	US-10-995-561-13233
C 13	16	80.0	251	3	US-09-960-352-3370
C 14	16	80.0	959	9	US-10-774-355A-815
C 15	16	80.0	966	9	US-10-774-355A-6
C 16	16	80.0	966	9	US-10-774-355A-8
C 17	15.8	79.0	249	9	US-10-425-115-114646

ALIGNMENTS

18	15.8	79.0	18	15.8	79.0	18	US-10-301-480-451748	Sequence 451748,
19	15.8	79.0	19	15.8	79.0	19	US-10-301-480-1065157	Sequence 1065157,
C 20	15.8	79.0	C 20	15.8	79.0	C 20	US-09-925-065A-741868	Sequence 741868,
C 21	15.8	79.0	C 21	15.8	79.0	C 21	US-09-925-065A-741868	Sequence 741868,
22	15.8	79.0	22	15.8	79.0	22	US-09-925-065A-382799	Sequence 382799,
23	15.8	79.0	23	15.8	79.0	23	US-09-925-065A-382799	Sequence 382799,
C 24	15.8	79.0	C 24	15.8	79.0	C 24	US-10-029-386-5570	Sequence 5570, Ap
C 25	15.8	79.0	C 25	15.8	79.0	C 25	US-10-301-480-73397	Sequence 73397, A
603	15.8	79.0	603	15.8	79.0	603	US-10-301-480-686806	Sequence 686806,
C 26	15.8	79.0	C 26	15.8	79.0	C 26	US-09-925-065A-805390	Sequence 805390,
614	15.8	79.0	614	15.8	79.0	614	US-09-925-065A-857799	Sequence 857799,
C 28	15.8	79.0	C 28	15.8	79.0	C 28	US-09-925-065A-805390	Sequence 805390,
C 29	15.8	79.0	C 29	15.8	79.0	C 29	US-09-925-065A-857799	Sequence 857799,
C 30	15.8	79.0	C 30	15.8	79.0	C 30	US-09-925-065A-857799	Sequence 857799,
614	15.8	79.0	614	15.8	79.0	614	US-10-027-632-261726	Sequence 261726,
31	15.8	79.0	31	15.8	79.0	31	US-10-027-632-261727	Sequence 261727,
32	15.8	79.0	32	15.8	79.0	32	US-10-027-632-261726	Sequence 261726,
33	15.8	79.0	33	15.8	79.0	33	US-10-027-632-261727	Sequence 261727,
614	15.8	79.0	614	15.8	79.0	614	US-10-301-480-96541	Sequence 96541, A
35	15.8	79.0	35	15.8	79.0	35	US-10-301-480-96542	Sequence 96542, A
36	15.8	79.0	36	15.8	79.0	36	US-10-301-480-709950	Sequence 709950,
37	15.8	79.0	37	15.8	79.0	37	US-10-301-480-709951	Sequence 709951,
38	15.8	79.0	38	15.8	79.0	38	US-10-301-480-52335	Sequence 52335, A
C 39	15.8	79.0	C 39	15.8	79.0	C 39	US-10-301-480-565744	Sequence 665744,
C 40	15.8	79.0	C 40	15.8	79.0	C 40	US-10-027-632-231799	Sequence 231799,
C 41	15.8	79.0	C 41	15.8	79.0	C 41	US-10-027-632-231799	Sequence 231799,
C 42	15.8	79.0	C 42	15.8	79.0	C 42	US-10-027-632-197818	Sequence 197818,
C 43	15.8	79.0	C 43	15.8	79.0	C 43	US-10-027-632-197818	Sequence 197818,
C 44	15.8	79.0	C 44	15.8	79.0	C 44	US-10-425-115-182124	Sequence 182124,
649	15.8	79.0	649	15.8	79.0	649	US-10-425-115-182124	Sequence 182124,

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 06:09:34 ; Search time 10.7733 Seconds  
(without alignments)  
2967.635 Million cell updates/sec

Title: US-10-600-642A-10

Perfect score: 20

Sequence: 1 cgtatccagagatggatatt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA\_New.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17	85.0	2917	6	US-10-449-902-24615	Sequence 24615, A
2	16.8	84.0	1680	9	US-11-056-3558-89398	Sequence 89398, A
3	16.8	84.0	1680	9	US-11-056-3558-93154	Sequence 93154, A
C 4	16.4	82.0	3541	6	US-10-449-902-22961	Sequence 22961, A
5	16.4	82.0	4886	6	US-10-449-902-26413	Sequence 26413, A
6	16.4	82.0	128963	6	US-10-540-898-86	Sequence 86, Appl
C 7	15.8	79.0	581	8	US-11-266-748A-102655	Sequence 102655, A
8	15.8	79.0	581	8	US-11-266-748A-15466	Sequence 15466, A
C 9	15.8	79.0	977	8	US-11-266-748A-188281	Sequence 188281, A
10	15.8	79.0	1149	8	US-11-266-748A-357159	Sequence 357159, A
11	15.8	79.0	1149	8	US-11-266-748A-440538	Sequence 440538, A
C 12	15.8	79.0	1167	8	US-11-217-529-78985	Sequence 78985, A
13	15.8	79.0	1452	6	US-10-449-902-6378	Sequence 6378, Ap
14	15.8	79.0	2182	9	US-11-218-305-13467	Sequence 13467, A
15	15.8	79.0	4246	6	US-10-449-902-12882	Sequence 12882, A
16	15.4	77.0	453	8	US-11-266-748A-429110	Sequence 429110, A
17	15.4	77.0	1229	9	US-11-218-305-7769	Sequence 7769, Ap
18	15.4	77.0	2134	6	US-10-449-902-25935	Sequence 25935, A
C 19	15.4	77.0	191584	6	US-10-539-228-800	Sequence 800, App
20	15.2	76.0	455	8	US-11-266-748A-57868	Sequence 57868, A
21	15.2	76.0	455	8	US-11-266-748A-209980	Sequence 209980, A
C 22	15.2	76.0	455	8	US-11-266-748A-234298	Sequence 234298, A
23	15.2	76.0	701	8	US-11-266-748A-54551	Sequence 54551, A

Sequence 195187, A  
Sequence 191104, A  
Sequence 225629, A  
Sequence 183704, A  
Sequence 191098, A  
Sequence 2784, Ap  
Sequence 5763, Ap  
Sequence 183710, A  
Sequence 191106, A  
Sequence 79167, A  
Sequence 20690, A  
Sequence 24865, A  
Sequence 23, Appl  
Sequence 37969, A  
Sequence 2885, Ap  
Sequence 171995, A  
Sequence 408954, A  
Sequence 198223, A  
Sequence 188372, A  
Sequence 22293, A  
Sequence 29845, A  
Sequence 250457, A

## ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:46:51 ; Search time 229.742 Seconds  
(without alignments)  
4868.007 Million cell updates/sec

Title: US-10-600-642A-10

Perfect score: 20

Sequence: 1 cgtatccagatgatatt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_est7:\*  
7: gb\_est8:\*  
8: gb\_est9:\*  
9: gb\_est10:\*  
10: gb\_est11:\*  
11: gb\_est12:\*  
12: gb\_est13:\*  
13: gb\_est14:\*  
14: gb\_est15:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	327	3	BW239100
2	17.4	87.0	330	3	BW241512
3	17.4	87.0	339	3	BW218663
C 4	17.4	87.0	427	10	DT586066
C 5	17.4	87.0	431	12	CC063142
C 6	17.4	87.0	442	11	AQ451583
C 7	17.4	87.0	555	1	AA439099
C 8	17.4	87.0	611	8	CR540685
C 9	17.4	87.0	655	14	AG184717
10	17.4	87.0	680	4	EX956933
11	17.4	87.0	734	14	AG604827
12	17.4	87.0	759	14	CR193190
C 13	17.4	87.0	765	11	AQ740400
14	17.4	87.0	776	9	DA572952
15	17.4	87.0	796	14	CR056044
16	17.4	87.0	807	9	DA572443
C 17	17.4	87.0	854	3	BW338401
18	17.4	87.0	920	14	CR025975
19	17.4	87.0	955	14	CNS003HX

20	17.4	87.0	1004	14	CNS002EM
21	17.4	87.0	1148	12	CC184031
22	17	85.0	298	1	AV038138
23	17	85.0	573	4	CB212402
24	17	85.0	608	8	CX112521
25	17	85.0	624	5	CK035277
26	17	85.0	694	4	CA285680
27	17	85.0	714	4	CA147700
28	17	85.0	1016	12	CC269065
C 29	16.8	84.0	393	11	B96101
C 30	16.8	84.0	481	11	AZ635587
C 31	16.8	84.0	509	14	CR173920
C 32	16.8	84.0	517	14	EX002160
C 33	16.8	84.0	519	11	AQ609367
C 34	16.8	84.0	524	11	BH205238
35	16.8	84.0	536	5	CD801621
36	16.8	84.0	539	1	AL914676
37	16.8	84.0	539	1	AL914677
38	16.8	84.0	549	5	CD800887
39	16.8	84.0	550	5	CD799281
C 40	16.8	84.0	558	3	BQ007296
41	16.8	84.0	578	11	BH743250
42	16.8	84.0	586	10	DM153237
43	16.8	84.0	626	3	BU259801
C 44	16.8	84.0	634	3	BW338401
45	16.8	84.0	644	3	BU133232

#### ALIGNMENTS

AL062407	Drosophil
CC184031	CH261-40A
AV038138	AV038138
CB212402	OML02682
CX112521	EI076H17
CK035277	36948raic
CA285680	SCEZSD108
CA147700	SCEZSD101
CC269065	CH261-119
B96101	P2303TRB IG
AZ635587	1M0493B05
CR173920	Reverse s
EX002160	Arabidops
AQ609367	HS-5068_B
BH205238	Sml-43C3
CD801621	EST 9530
AL914676	AL914676
AL914677	AL914677
CD800887	EST 14132
CD799281	EST 12942
BQ007296	UI-1-BC0-
BH743250	Gz71C10-G
DM153237	CLVX505.b
BU259801	603502542
BW338401	BW338401
BU133232	603120762

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:39:06 ; Search time 7136.34 Seconds  
 (without alignments)  
 5591.547 Million cell updates/sec

Title: US-10-600-642A-1  
 Perfect score: 624  
 Sequence: 1 gaagtcgtacaaggtagcc.....agcggttatggaaggttaa 624

Scoring table: IDENTITY NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

## Database :

## ALIGNMENTS

GenEmbl:\*

1: gb\_env:\*

2: gb\_pat:\*

3: gb\_ph:\*

4: gb\_pl:\*

5: gb\_pr:\*

6: gb\_ro:\*

7: gb\_ats:\*

8: gb\_sy:\*

9: gb\_un:\*

10: gb\_vi:\*

11: gb\_ov:\*

12: gb\_htg:\*

13: gb\_in:\*

14: gb\_om:\*

15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	624	2 E54411	E54411 Specific an
2	624	100.0	624	2 AR408838	AR408838 Sequence
3	624	100.0	624	15 AB022063	AB022063 Pectinatu
4	318.8	51.1	724	2 E54413	E54413 Specific an
5	318.8	51.1	724	2 AR408840	AR408840 Sequence
6	318.8	51.1	724	15 AB022061	AB022061 Pectinatu
7	318.2	51.0	442	2 E54412	E54412 Specific an
8	318.2	51.0	442	2 AR408839	AR408839 Sequence
9	318.2	51.0	442	2 AB022064	AB022064 Pectinatu
10	142.6	22.9	579	2 E34162	E34162 Gene for de
11	142.6	22.9	579	15 AB022094	AB022094 Selenomon
12	133.6	21.4	110000	15 AE015927_05	Continuation (6 of
13	132.6	21.2	5996	15 CJ16SRNA	Z29326 C.Jejuni TG
14	132.6	21.2	110000	15 CP000025_00	CP000025 Campyloba
15	132.6	21.2	110000	15 CP000025_04	Continuation (5 of
16	132.6	21.2	110000	15 CP000025_07	Continuation (8 of
17	132.6	21.2	308601	15 CJ11168X2	AL139075 Campyloba
18	132.6	21.2	314150	15 CJ11168X1	AL139074 Campyloba

19	132.6	21.2	317511	15	CJ11168X3
20	132.4	21.2	535	1	AY899800
21	129.6	20.8	417	15	AB040726
22	128.8	20.6	6431	15	AE013169
23	126.2	20.2	413	15	AB040729
24	122.6	19.6	467	15	AB040727
25	122.2	19.6	514	15	AB040737
26	122.2	19.6	6696	15	AB045289
27	122.2	19.6	7487	15	AB211985
28	122.2	19.6	7878	15	AB045291
29	122.2	19.6	110000	15	BA000016_25
30	121	19.4	467	15	AB040730
31	121	19.4	968	15	AF146727
32	121	19.4	2109	1	DQ011252
33	121	19.4	2110	1	DQ011251
34	119.8	19.1	460	15	AB040723
35	117.8	18.9	556	15	AB040720
36	117.2	18.8	2423	15	AB066098
37	117	18.8	1005	15	AJ936965
38	117	18.8	2020	15	AY288082
39	117	18.8	2020	15	AY288083
40	117	18.8	2021	15	AY288080
41	117	18.8	2163	15	AF123093
42	117	18.8	2164	15	AF123088
43	117	18.8	2165	15	AF442743
44	116.8	18.7	734	1	AB198400
45	116.8	18.7	2020	15	AY288081

AL139076 Campyloba  
 AY899800 Unculture  
 AB040726 Clostridi  
 AE013169 Thermoana  
 AB040729 Clostridi  
 AB040727 Clostridi  
 AB040737 Clostridi  
 AB045289 Clostridi  
 AB211985 Campyloba  
 AB045291 Clostridi  
 Continuation (26 o  
 AB040730 Clostridi  
 AF146727 Campyloba  
 DQ011252 Unculture  
 DQ011251 Unculture  
 AB040723 Clostridi  
 AB040720 Clostridi  
 AB066098 Campyloba  
 AJ936965 Xanthomon  
 AY288082 Xanthomon  
 AY288083 Xanthomon  
 AY288080 Xanthomon  
 AF123093 Xanthomon  
 AF123088 Xanthomon  
 AF442743 Xanthomon  
 AB198400 Unculture  
 AY288081 Xanthomon

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:30:09 ; Search time 901.888 Seconds  
(without alignments)  
4823.973 Million cell updates/sec

Title: US-10-600-642A-1  
Perfect score: 624  
Sequence: 1 gaagtcgtacaagtagcc.....agcggttatggaagttaa 624

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005s:\*  
15: Geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	624	3	Aaz91771 Spacer re
2	624	100.0	624	4	Aai71855 Pectinatu
3	318.8	51.1	724	3	Aaz91773 Spacer re
4	318.8	51.1	724	4	Aai71857 Pectinatu
5	318.2	51.0	442	3	Aaz91772 Spacer re
6	318.2	51.0	442	4	Aai71856 Pectinatu
7	142.6	22.9	579	3	Aaa39326 S. lactic
8	116.6	18.7	399	3	Aaz91774 Spacer re
9	116.6	18.7	399	4	Aai71858 Pectinatu
10	114.2	18.3	425	10	Adell108 Acidovora
11	112.4	18.0	670	10	Adell114 Xanthomon
12	99.4	15.9	65589	6	ABA30521_23 Continuation (24 o
13	99.4	15.9	110000	6	ABA30521_05 Continuation (6 of
14	99.4	15.9	110000	6	ABA30521_19 Continuation (20 o
15	99.4	15.9	110000	6	ABA30521_22 Continuation (23 o
16	97.8	15.7	1069	2	Aax13806 Enterococ
17	97.8	15.7	1069	6	AbS99601 Enterococ
18	91.4	14.6	681	4	Aah50334 Bacterial

19	86	13.8	488	10	ADC53887	Adc53887 Pediococ
20	85.6	13.7	339	2	AAV02628	AAV02628 S. simula
21	84.6	13.6	479	5	AAI71400	AAI71400 Pediococ
22	84.4	13.5	370	2	AAV78592	AAV78592 Staphyloc
23	84.4	13.5	400	2	AAV78196	AAV78196 Staphyloc
24	84.4	13.5	400	2	AAV78159	AAV78159 Staphyloc
25	84.4	13.5	487	2	AAV77924	AAV77924 Staphyloc
26	84.4	13.5	1785	2	AAV77317	AAV77317 Staphyloc
27	84.4	13.5	5973	14	ADM94079	ADM94079 Staphyloc
28	84.2	13.5	383	2	AAI11850	AAI11850 S. aureus
29	84.2	13.5	460	2	AAV02624	AAV02624 S. aureus
30	84	13.5	323	2	AAV78650	AAV78650 Staphyloc
31	83	13.3	2331	14	ABE42738	ABE42738 L. pneumo
32	83	13.3	105295	14	ABE35712	ABE35712 L. pneumo
33	83	13.3	110000	14	ABE39175_04	Continuation (5 of
34	83	13.3	110000	14	ABE39175_06	Continuation (7 of
35	83	13.3	298667	14	ABE39173	Continuation (7 of
36	82.4	13.2	240	2	AAV78887	ABE39173 L. pneumo
37	82.2	13.2	400	2	AAV78121	AAV78887 Staphyloc
38	81.8	13.1	195	10	ADC92601	AAV78121 Staphyloc
39	81.4	13.0	110000	14	ABE42401_04	ADC92601 E. faeciu
40	81.4	13.0	110000	14	ABE42401_06	Continuation (5 of
41	79.6	12.8	1311	2	AAV77852	Continuation (7 of
42	79.4	12.7	591	3	AAA39330	AAV77852 Staphyloc
43	79.2	12.7	1781	14	ACL63717	Aaa39330 Z. raffin
44	79.2	12.7	3937	4	AAH54408	ACL63717 M. xanthu
45	78	12.5	7291	14	ADM94182	AAH54408 S. epider
						ADM94182 Staphyloc

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:57:34 ; Search time 264.021 Seconds  
(without alignments)  
4422.263 Million cell updates/sec

Title: US-10-600-642A-1

Perfect score: 624

Sequence: 1 gaagtcgtacaagtagcc.....agcggttatggaagttaa 624

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PC/US COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	624	100.0	624	3	US-09-762-633-1 Sequence 1, Appli
2	318.8	51.1	724	3	US-09-762-633-3 Sequence 3, Appli
3	318.2	51.0	442	3	US-09-762-633-2 Sequence 2, Appli
4	116.6	18.7	339	3	US-09-762-633-4 Sequence 4, Appli
5	85.6	13.7	339	3	US-08-607-384A-9 Sequence 9, Appli
C 6	84.4	13.5	370	3	US-08-956-171B-4281 Sequence 4281, Ap
C 7	84.4	13.5	370	3	US-08-781-986A-4281 Sequence 4281, Ap
C 8	84.4	13.5	400	3	US-08-956-171B-3848 Sequence 3848, Ap
C 9	84.4	13.5	400	3	US-08-956-171B-3885 Sequence 3885, Ap
C 10	84.4	13.5	400	3	US-08-781-986A-3848 Sequence 3848, Ap
C 11	84.4	13.5	400	3	US-08-781-986A-3885 Sequence 3885, Ap
C 12	84.4	13.5	487	3	US-08-956-171B-3613 Sequence 3613, Ap
C 13	84.4	13.5	487	3	US-08-781-986A-3613 Sequence 3613, Ap
C 14	84.4	13.5	1785	3	US-08-956-171B-3006 Sequence 3006, Ap
15	84.4	13.5	1785	3	US-08-781-986A-3006 Sequence 3006, Ap
16	84.2	13.5	383	3	US-08-765-332-142 Sequence 142, App
17	84.2	13.5	383	3	US-09-448-894-142 Sequence 142, App
18	84.2	13.5	383	3	US-09-931-486-142 Sequence 142, App
19	84.2	13.5	460	2	US-08-607-384A-5 Sequence 5, Appli
C 20	84	13.5	323	3	US-08-956-171B-4339 Sequence 4339, Ap
C 21	84	13.5	323	3	US-08-781-986A-4339 Sequence 4339, Ap
C 22	82.4	13.2	240	3	US-08-956-171B-4576 Sequence 4576, Ap
C 23	82.4	13.2	240	3	US-08-781-986A-4576 Sequence 4576, Ap

#### ALIGNMENTS

c 24	82.2	13.2	400	3	US-08-956-171B-3810	Sequence 3810, Ap
c 25	82.2	13.2	400	3	US-08-781-986A-3810	Sequence 3810, Ap
26	81.8	13.1	195	3	US-09-107-532A-2228	Sequence 2228, Ap
27	79.6	12.8	1311	3	US-08-956-171B-3541	Sequence 3541, Ap
28	79.6	12.8	1311	3	US-08-781-986A-3541	Sequence 3541, Ap
29	79.2	12.7	1781	3	US-09-902-540-180	Sequence 180, App
30	79.2	12.7	3937	3	US-09-710-279-3772	Sequence 3772, Ap
31	76.6	12.3	343	3	US-08-956-171B-4181	Sequence 4181, Ap
32	76.6	12.3	343	3	US-08-781-986A-4181	Sequence 4181, Ap
C 33	76.6	12.3	400	3	US-08-956-171B-3583	Sequence 3583, Ap
C 34	76.6	12.3	400	3	US-08-956-171B-3591	Sequence 3591, Ap
C 35	76.6	12.3	400	3	US-08-956-171B-3591	Sequence 3591, Ap
C 36	76.6	12.3	400	3	US-08-956-171B-3608	Sequence 3608, Ap
C 37	76.6	12.3	400	3	US-08-956-171B-3643	Sequence 3643, Ap
C 38	76.6	12.3	400	3	US-08-781-986A-3583	Sequence 3583, Ap
C 39	76.6	12.3	400	3	US-08-781-986A-3591	Sequence 3591, Ap
C 40	76.6	12.3	400	3	US-08-781-986A-3608	Sequence 3608, Ap
C 41	76.6	12.3	400	3	US-08-781-986A-3643	Sequence 3643, Ap
C 42	76.6	12.3	400	3	US-08-781-986A-3711	Sequence 3711, Ap
C 43	76.2	12.2	381	3	US-08-956-171B-3754	Sequence 3754, Ap
C 44	76.2	12.2	381	3	US-08-781-986A-3754	Sequence 3754, Ap
C 45	75.6	12.1	400	3	US-08-956-171B-3821	Sequence 3821, Ap

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 06:08:00 ; Search time 3132.2 Seconds  
(without alignments)  
2447.953 Million cell updates/sec

Title: US-10-600-642A-1

Perfect score: 624

Sequence: 1 Gaagtcgtacaaggtagcc.....agcggttatggaagttaa 624

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	624	8	US-10-600-642-1
2	318.8	51.1	724	8	US-10-600-642-3
3	218.2	51.0	442	8	US-10-600-642-2
4	116.6	18.7	399	8	US-10-600-642-4
5	114.2	18.3	425	13	US-11-112-257-32
6	114.2	18.3	425	13	US-11-112-257-32
7	112.4	18.0	670	7	US-10-397-551-38
8	112.4	18.0	670	13	US-11-112-257-38
9	111	17.8	2731748	8	US-10-297-465A-1
10	97.8	15.7	1069	3	US-09-070-927A-869
11	84.4	13.5	370	2	US-08-781-986A-4281
12	84.4	13.5	370	8	US-10-329-624-4281
13	84.4	13.5	400	2	US-08-781-986A-3848
14	84.4	13.5	400	2	US-08-781-986A-3885
15	84.4	13.5	400	8	US-10-329-624-3848
16	84.4	13.5	400	8	US-10-329-624-3885
17	84.4	13.5	487	2	US-08-781-986A-3613

Sequence 3613, Ap	487	13.5	84.4	8	US-10-329-624-3613
Sequence 3006, Ap	1785	13.5	84.4	2	US-08-781-986A-3006
Sequence 3006, Ap	1785	13.5	84.4	2	US-10-329-624-3006
Sequence 13, Appl	5973	13.5	84.4	9	US-10-857-625-13
Sequence 142, Appl	383	13.5	84.2	3	US-09-931-486-142
Sequence 142, Appl	383	13.5	84.2	10	US-10-895-114-142
Sequence 4339, Ap	323	13.5	84	2	US-08-781-986A-4339
Sequence 4339, Ap	323	13.5	84	8	US-10-329-624-4339
Sequence 4576, Ap	240	13.2	82.4	8	US-08-781-986A-4576
Sequence 4576, Ap	240	13.2	82.4	2	US-10-329-624-4576
Sequence 3810, Ap	400	13.2	82.2	8	US-08-781-986A-3810
Sequence 3810, Ap	400	13.2	82.2	2	US-10-329-624-3810
Sequence 3541, Ap	1311	12.8	79.6	2	US-08-781-986A-3541
Sequence 3541, Ap	1311	12.8	79.6	8	US-10-329-624-3541
Sequence 3772, Ap	3937	12.7	79.2	10	US-10-793-626-3772
Sequence 116, Appl	7291	12.5	78	3	US-10-857-625-116
Sequence 1377, Ap	255	12.3	76.6	3	US-09-815-242-1377
Sequence 1402, Ap	255	12.3	76.6	3	US-09-815-242-1402
Sequence 1415, Ap	255	12.3	76.6	3	US-09-815-242-1415
Sequence 1423, Ap	255	12.3	76.6	3	US-09-815-242-1423
Sequence 1431, Ap	255	12.3	76.6	3	US-09-815-242-1431
Sequence 1454, Ap	255	12.3	76.6	3	US-09-815-242-1454
Sequence 1459, Ap	255	12.3	76.6	3	US-09-815-242-1459
Sequence 1473, Ap	255	12.3	76.6	3	US-09-815-242-1473
Sequence 1475, Ap	255	12.3	76.6	3	US-09-815-242-1475
Sequence 1544, Ap	255	12.3	76.6	3	US-09-815-242-1544
Sequence 1638, Ap	255	12.3	76.6	3	US-09-815-242-1638
Sequence 4181, Ap	343	12.3	76.6	2	US-08-781-986A-4181

#### ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 06:09:34 ; Search time 336.128 Seconds  
(without alignments)  
2967.635 Million cell updates/sec

Title: US-10-600-642A-1  
Perfect score: 624  
Sequence: 1 gaagtcgtacaagtagcc.....agcggttatggaagttaa 624

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	75.8	12.1	26683	9	US-11-021-837-26
C 2	70.6	11.3	77	9	US-11-348-413-10826
C 3	68	10.9	39013	9	US-11-021-837-30
4	66	10.6	556	8	US-11-238-162-10
5	66	10.6	603	8	US-11-238-162-11
6	65.8	10.5	201	8	US-11-266-748A-416742
7	62.8	10.1	472	8	US-11-238-162-5
C 8	62.6	10.0	274050	6	US-10-550-787-5
9	62.4	10.0	471	8	US-11-238-162-4
10	62.4	10.0	473	8	US-11-238-162-3
11	61	9.8	584	8	US-11-238-162-7
12	60.2	9.6	503	8	US-11-266-748A-206328
13	60	9.6	4294	9	US-11-021-837-14
14	57.4	9.2	77	9	US-11-348-413-18
15	57.2	9.2	536	8	US-11-256-428-67
16	56	9.0	17395	9	US-11-021-837-52
17	55.2	8.8	76	9	US-11-348-413-10833
18	52.8	8.5	1554	9	US-11-348-413-10825
19	52.4	8.4	1000	8	US-11-266-748A-206971
C 20	52.2	8.4	1000	8	US-11-266-748A-206292
21	50.4	8.1	76	9	US-11-348-413-1
C 22	49.6	7.9	228	9	US-11-348-413-13042
23	47.2	7.6	76	9	US-11-348-413-10842

Sequence 18, Appl  
Sequence 2950, Ap  
Sequence 12, Appl  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 40, Appl  
Sequence 195038,  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 10845, A  
Sequence 44347, A  
Sequence 5845, Ap  
Sequence 17141, A

21159 9 US-11-021-837-18  
1950 6 US-10-449-902-2950  
1538 9 US-11-348-413-12  
1452 6 US-10-511-345A-1  
1531 8 US-11-256-221-1  
5048 7 US-11-338-847-2  
73 9 US-11-348-413-2  
1000 8 US-11-233-726-40  
704 8 US-11-266-748A-195038  
1526 9 US-11-350-955-4  
1528 9 US-11-350-955-2  
1528 9 US-11-350-796-2  
1529 9 US-11-350-955-3  
1532 9 US-11-350-955-1  
1532 9 US-11-350-796-1  
76 9 US-11-348-413-10846  
902 8 US-11-266-748A-44347  
1542 8 US-11-331-987-3  
74 9 US-11-348-413-5845  
74 9 US-11-348-413-17141

## ALIGNMENTS



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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:46:51 ; Search time 7167.96 Seconds  
(without alignments)  
4868.007 Million cell updates/sec

Title: US-10-600-642A-1  
Perfect score: 624  
Sequence: 1 gaagtcgtaacaagtagcc.....agcgttatggaagttaa 624

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_est7:\*  
7: gb\_est8:\*  
8: gb\_est9:\*  
9: gb\_est10:\*  
10: gb\_est11:\*  
11: gb\_est12:\*  
12: gb\_est13:\*  
13: gb\_est14:\*  
14: gb\_est15:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	107.8	17.3	810	12	CC123417 NDL.73C23
C 2	97.8	15.7	809	13	CZ191243 305 GFE00
C 3	97.8	15.7	6499	11	BH771024 LLMGtag74
4	80.2	12.9	968	14	DU735358 APK13214
5	77.2	12.4	894	14	DU768642 APKG1053
6	76.6	12.3	288	5	CD518612 AGENCOURT
7	74	11.9	909	14	DU748135 ASNC417.g
C 8	70.4	11.3	351	14	AG267606 Cyanidios
9	69.8	11.2	928	14	DU794311 APKH5418
C 10	69.4	11.1	631	11	BH861078 S14H6SP6
11	69.4	11.1	635	11	BH861097 BLE12T7 W
C 12	66	10.6	911	14	DU741053 APK16052
C 13	65.8	10.5	287	11	BH614410 1C22AG2 S
C 14	65.2	10.4	886	14	AG879127 Oryza sat
C 15	64.6	10.4	818	11	BZ554413 pacel-60
C 16	64.6	10.4	823	12	BZ566461 pacel-164
C 17	64.6	10.4	1352	12	BZ577091 msh2_5245
C 18	64.2	10.3	261	5	CF843831 psHB043xi
19	64.2	10.3	525	3	BP490032 BP490032

# ALIGNMENTS

C 20	63.8	10.2	639	11	AQ509640
C 21	63	10.1	960	14	DU778616
C 22	62.2	10.0	371	13	CZ191241
C 23	62.2	10.0	774	13	CL965162
C 24	61.8	9.9	507	11	BH200120
C 25	61.8	9.9	629	11	BH201541
26	61	9.8	487	8	CV953459
27	61	9.8	501	3	BP911902
28	61	9.8	536	8	CV911301
29	61	9.8	563	8	CV904243
30	61	9.8	648	8	CV950720
31	61	9.8	672	8	CV947986
C 32	60.2	9.6	853	14	DU783531
C 33	60	9.6	1335	12	BZ576949
C 34	59.4	9.5	870	11	BZ556251
C 35	59	9.5	390	5	CK339707
C 36	59	9.5	619	1	AA680996
C 37	58.6	9.4	992	14	DU753122
38	58.4	9.4	601	11	BH861047
C 39	58	9.3	191	11	AZ578476
C 40	57.8	9.3	866	14	DU783720
C 41	57.8	9.3	993	14	DU752455
C 42	57.6	9.2	868	11	BH814965
C 43	57.6	9.2	1143	11	BH814966
44	57.4	9.2	723	9	DN616068
C 45	57.4	9.2	970	14	DU740944

AQ509640 nbxb0096P  
DU778616 ASXB2276.  
CZ191241 328 GFE00  
CL965162 OeIFC011  
BH200120 Sm1-57J2  
BH201541 Sm1-57P13  
CV953459 PWRPwa\_01  
BP911902 BP911902  
CV911301 PE025C3 m  
CV904243 PD044F4 m  
CV950720 PVTPvb\_42  
CV947986 PVTPvb\_11  
DU783531 HF500\_06  
BZ576949 msh2\_5177  
BZ556251 pacel-60  
CK339707 C0862C08-  
AA680996 SM3D9CA51  
DU753122 ASNF2962.  
BH861047 N14A7T7 W  
AZ578476 23h03 Sho  
DU783720 HF500\_12  
DU752455 ASNF2588-  
BH814965 BPC5 Mai  
BH814966 BPC15 Ma  
DN616068 SPM5A5 Sa  
DU740944 APK16003.

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:39:06 ; Search time 5054.91 Seconds  
(without alignments)  
5591.547 Million cell updates/sec

Title: US-10-600-642A-2

Perfect score: 442

Sequence: 1 gaagtcgtaacaaggtagcc.....agcgggtatgaaaagttaa 442

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710535 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	442	100.0	442	2	E54412
2	442	100.0	442	2	AR408839
3	442	100.0	442	15	AB022064
4	318.2	72.0	624	2	E54411
5	318.2	72.0	624	2	AR408838
6	318.2	72.0	624	15	AB022063
7	208.6	47.2	399	2	E54414
8	208.6	47.2	399	2	AR408841
9	208.6	47.2	399	15	AB022062
10	163.8	37.1	724	2	E54413
11	163.8	37.1	724	2	AR408840
12	163.8	37.1	724	15	AB022061
13	77.4	17.5	520	15	AF080100
14	74.6	16.9	1875	15	ED1301829
15	74.4	16.8	1701	15	EMA301835
16	70.6	16.0	3328	15	AF401673
17	70.6	16.0	84661	15	CR936503_18
18	70.6	16.0	110000	15	CR936503_02

c	19	70.6	16.0	110000	15	CR936503_03	Continuation (4 of
	20	70.6	16.0	110000	15	CR936503_04	Continuation (5 of
	21	70.6	16.0	110000	15	CR936503_15	Continuation (16 of
c	22	69	15.6	284	2	BD016456	BD16456 Oligonucle
	23	69	15.6	477	1	AB198420	AB198420 Unculture
	24	68.2	15.4	7218	2	I66494	I66494 Sequence 14
c	25	68	15.4	560	15	AF429604	AF429604 Lactobac
	26	67.8	15.3	474	15	AF478106	AF478106 Faenibaci
	27	67.8	15.3	528	15	AF405382	AF405382 Pediococ
	28	67.8	15.3	534	15	AF405366	AF405366 Pediococ
	29	67.8	15.3	534	15	AF405384	AF405384 Pediococ
	30	67.6	15.3	534	15	AF405367	AF405367 Pediococ
	31	67.4	15.2	531	15	AF405365	AF405365 Pediococ
	32	67.4	15.2	535	15	AF405359	AF405359 Pediococ
	33	67.4	15.2	536	15	AF405358	AF405358 Pediococ
	34	66.8	15.1	552	15	AB083115	AB083115 Lactobaci
	35	66.8	15.1	110000	15	AE017194_03	Continuation (4 of
	36	66.6	15.1	4566	15	AB019250	AB019250 Erysipel
	37	66.6	15.1	4865	15	AB019248	AB019248 Erysipel
	38	65.8	14.9	4867	15	AB019247	AB019247 Erysipel
	39	65.2	14.8	497	15	AY008265	AY008265 Bacillus
	40	65.2	14.8	509	15	AF293851	AF293851 Bacillus
	41	65.2	14.8	110000	15	AE016879_00	AE016879 Bacillus
	42	65.2	14.8	110000	15	AE016879_01	Continuation (2 of
	43	65.2	14.8	110000	15	AE016879_02	Continuation (3 of
	44	65.2	14.8	110000	15	AE016879_05	Continuation (6 of
	45	65.2	14.8	110000	15	AE016879_07	Continuation (8 of

ALIGNMENTS

Continuation (4 of  
Continuation (5 of  
Continuation (16 of  
BD016456 Oligonucle  
AB198420 Unculture  
I66494 Sequence 14  
AF429604 Lactobaci  
AF478106 Paenibaci  
AF405382 Pediococcc  
AF405366 Pediococcc  
AF405384 Pediococcc  
AF405367 Pediococcc  
AF405365 Pediococcc  
AF405359 Pediococcc  
AF405358 Pediococcc  
AB083115 Lactobaci  
Continuation (4 of  
AB019250 Erysipel  
AB019248 Erysipel  
AB019247 Erysipel  
AY008265 Bacillus  
AF293851 Bacillus  
AE016879 Bacillus  
Continuation (2 of  
Continuation (3 of  
Continuation (6 of  
Continuation (8 of

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:30:09 ; Search time 638.837 Seconds  
(without alignments)  
4823.973 Million cell updates/sec

Title: US-10-600-642A-2  
Perfect score: 442  
Sequence: 1 gaagtcgtacaagtagcc.....agcggttatggaagttaa 442

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_8.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	442	100.0	442	3	Aaz91772 Spacer re
2	442	100.0	442	4	Aai71856 Pectinatu
3	318.2	72.0	624	3	Aaz91771 Spacer re
4	318.2	72.0	624	4	Aai71855 Pectinatu
5	208.6	47.2	399	3	Aaz91774 Spacer re
6	208.6	47.2	399	4	Aai71858 Pectinatu
7	163.8	37.1	724	3	Aaz91773 Spacer re
8	163.8	37.1	724	4	Aai71857 Pectinatu
9	69	15.6	284	5	Aai71401 Pediococc
10	67.4	15.2	291	10	ADC53888
11	64.2	14.5	538	13	ADU78344 Lactobaci
12	63.2	14.3	753	4	AAC88675 Interjeni
13	63.2	14.3	753	6	ABS52493 Acidovora
14	62.4	14.1	110000	9	ADB12064 Alloiococ
15	62.4	14.1	110000	9	ADB12064_05
16	62.2	14.1	526	10	ADE11115 Erwinia t
17	61.8	14.0	1069	2	AAX13806 Enterococ
18	61.8	14.0	1069	6	ABS99601 Enterococ

19	61.8	14.0	2996	12	ADH50160	Adh50160 Bacterial
20	61.8	14.0	110000	9	ADB12064_04	Continuation (5 of
C 21	61.8	14.0	110000	9	ADB12064_14	Continuation (15 o
C 22	61.8	14.0	110000	9	ADB12064_15	Continuation (16 o
23	61.6	13.9	414	2	AAQ62078	Aaq62078 Lactobaci
24	61.6	13.9	414	2	AAQ88211	Aaq88211 Lactobaci
25	61.6	13.9	540	2	AAQ62072	Aaq62072 L. hetero
26	61.6	13.9	540	2	AAQ88205	Aaq88205 Lactobaci
27	61.6	13.9	585	2	AAQ62079	Aaq62079 L. brevis
28	61.6	13.9	585	2	AAQ88212	Aaq88212 Lactobaci
C 29	61	13.8	614	13	ADU78345	Adu78345 Streptoco
C 30	60.8	13.8	65589	6	ABA90521_23	Continuation (24 o
31	60.8	13.8	110000	6	ABA90521_05	Continuation (6 of
C 32	60.8	13.8	110000	6	ABA90521_19	Continuation (20 o
C 33	60.8	13.8	110000	6	ABA90521_22	Continuation (23 o
34	60.6	13.7	294	10	ADC53892	Adc53892 Pediococc
35	60.6	13.7	294	10	ADC53890	Adc53890 Pediococc
36	60.6	13.7	4259	13	ADV87716	Adv87716 Streptoco
37	60.6	13.7	4259	13	ADV78969	Adv78969 Streptoco
C 38	60.6	13.7	7250	6	ABN72583	Abn72583 Streptoco
C 39	60.6	13.7	7267	6	ABN72580	Abn72580 Streptoco
C 40	60.6	13.7	7361	6	ABN72578	Abn72578 Streptoco
C 41	60.6	13.7	7392	6	ABN72582	Abn72582 Streptoco
C 42	60.6	13.7	8172	6	ABN72579	Abn72579 Streptoco
C 43	60.6	13.7	8766	6	ABN72581	Abn72581 Streptoco
C 44	60.6	13.7	9042	6	ABN72584	Abn72584 Streptoco
C 45	60.6	13.7	55561	6	ABN71527_21	Continuation (22 o

#### ALIGNMENTS

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:57:34 ; Search time 187.015 Seconds  
(without alignments)  
4422.263 Million cell updates/sec

Title: US-10-600-642A-2

Perfect score: 442

Sequence: 1 gaagtcgtacaagtagcc.....agcggtatgaaagttaa 442

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:\*
- 1: /EMC Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*
  - 2: /EMC Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*
  - 3: /EMC Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*
  - 4: /EMC Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*
  - 5: /EMC Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*
  - 6: /EMC Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*
  - 7: /EMC Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*
  - 8: /EMC Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*
  - 9: /EMC Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*
  - 10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	442	100.0	442	3	US-09-762-633-2
2	318.2	72.0	624	3	US-09-762-633-1
3	208.6	47.2	399	3	US-09-762-633-4
4	163.8	37.1	724	3	US-09-762-633-3
5	68.2	15.4	7218	2	US-08-232-463-14
6	63.2	14.3	753	3	US-09-393-877-9
7	63.2	14.3	753	3	US-09-703-807-9
8	60.4	13.7	261	3	US-09-583-110-1038
9	60.4	13.7	261	3	US-09-583-110-1763
10	60	13.6	251	3	US-08-956-171E-4521
11	60	13.6	251	3	US-08-781-986A-4521
12	60	13.6	322	3	US-08-956-171E-4395
13	60	13.6	322	3	US-08-781-986A-4395
14	60	13.6	333	3	US-08-956-171E-4473
15	60	13.6	333	3	US-08-781-986A-4473
16	60	13.6	362	3	US-08-956-171E-4147
17	60	13.6	362	3	US-08-781-986A-4147
18	60	13.6	389	3	US-08-956-171E-3950
19	60	13.6	389	3	US-08-781-986A-3950
20	60	13.6	400	3	US-08-956-171E-3583
21	60	13.6	400	3	US-08-781-986A-3583
22	60	13.6	400	3	US-08-956-171E-3617
23	60	13.6	400	3	US-08-781-986A-3617

c	24	60	13.6	400	3	US-08-956-171E-3689	Sequence 3689, Ap
c	25	60	13.6	400	3	US-08-956-171E-3697	Sequence 3697, Ap
c	26	60	13.6	400	3	US-08-956-171E-3711	Sequence 3711, Ap
c	27	60	13.6	400	3	US-08-956-171E-3716	Sequence 3716, Ap
c	28	60	13.6	400	3	US-08-956-171E-3758	Sequence 3758, Ap
c	29	60	13.6	400	3	US-08-956-171E-3810	Sequence 3810, Ap
c	30	60	13.6	400	3	US-08-956-171E-3820	Sequence 3820, Ap
c	31	60	13.6	400	3	US-08-956-171E-3832	Sequence 3832, Ap
c	32	60	13.6	400	3	US-08-956-171E-3885	Sequence 3885, Ap
c	33	60	13.6	400	3	US-08-956-171E-3885	Sequence 3885, Ap
c	34	60	13.6	400	3	US-08-956-171E-3922	Sequence 3922, Ap
c	35	60	13.6	400	3	US-08-956-171E-3938	Sequence 3938, Ap
c	36	60	13.6	400	3	US-08-956-171E-4126	Sequence 4126, Ap
c	37	60	13.6	400	3	US-08-781-986A-3583	Sequence 3583, Ap
c	38	60	13.6	400	3	US-08-781-986A-3608	Sequence 3608, Ap
c	39	60	13.6	400	3	US-08-781-986A-3617	Sequence 3617, Ap
c	40	60	13.6	400	3	US-08-781-986A-3637	Sequence 3637, Ap
c	41	60	13.6	400	3	US-08-781-986A-3689	Sequence 3689, Ap
c	42	60	13.6	400	3	US-08-781-986A-3697	Sequence 3697, Ap
c	43	60	13.6	400	3	US-08-781-986A-3711	Sequence 3711, Ap
c	44	60	13.6	400	3	US-08-781-986A-3716	Sequence 3716, Ap
c	45	60	13.6	400	3	US-08-781-986A-3758	Sequence 3758, Ap

## ALIGNMENTS

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 06:08:00 ; Search time 2218.64 Seconds  
(without alignments)  
2447.953 Million cell updates/sec

Title: US-10-600-642A-2

Perfect score: 442

Sequence: 1 gaagtgcatacaaggtagcc.....agcgttatggaagtttaa 442

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	442	100.0	442	8	US-10-600-642-2
2	318.2	72.0	624	8	US-10-600-642-1
3	208.6	47.2	399	8	US-10-600-642-4
4	163.8	37.1	724	8	US-10-600-642-3
5	62.4	14.1	1754382	10	US-10-501-282-6651
C 6	62.4	14.1	1754382	10	US-10-501-282-6651
7	62.2	14.1	526	7	US-10-397-551-39
8	62.2	14.1	526	13	US-11-112-257-39
C 9	61.8	14.0	1069	3	US-09-070-327A-869
10	60.4	13.7	2162598	9	US-10-472-928-4979
C 11	60.4	13.7	2162598	9	US-10-472-928-4979
C 12	60	13.6	251	2	US-08-781-986A-4521
C 13	60	13.6	251	8	US-10-329-624-4521
C 14	60	13.6	252	8	US-10-282-122A-5323
C 15	60	13.6	322	2	US-08-781-986A-4395
C 16	60	13.6	322	8	US-10-329-624-4395
C 17	60	13.6	333	2	US-08-781-986A-4473

60	13.6	333	8	US-10-329-624-4473	Sequence 4473, Ap
60	13.6	362	2	US-08-781-986A-4147	Sequence 4147, Ap
60	13.6	362	8	US-10-329-624-4147	Sequence 4147, Ap
60	13.6	379	3	US-09-815-242-2479	Sequence 2479, Ap
60	13.6	379	3	US-09-815-242-2501	Sequence 2501, Ap
60	13.6	379	8	US-10-282-122A-5007	Sequence 5007, Ap
60	13.6	379	8	US-10-282-122A-5030	Sequence 5030, Ap
60	13.6	389	2	US-08-781-986A-3950	Sequence 3950, Ap
60	13.6	389	8	US-10-329-624-3950	Sequence 3950, Ap
60	13.6	395	3	US-09-815-242-1811	Sequence 1811, Ap
60	13.6	395	3	US-09-815-242-1859	Sequence 1859, Ap
60	13.6	395	8	US-10-282-122A-4382	Sequence 4382, Ap
60	13.6	395	8	US-10-282-122A-4383	Sequence 4383, Ap
60	13.6	400	2	US-08-781-986A-3583	Sequence 3583, Ap
60	13.6	400	2	US-08-781-986A-3608	Sequence 3608, Ap
60	13.6	400	2	US-08-781-986A-3617	Sequence 3617, Ap
60	13.6	400	2	US-08-781-986A-3637	Sequence 3637, Ap
60	13.6	400	2	US-08-781-986A-3689	Sequence 3689, Ap
60	13.6	400	2	US-08-781-986A-3697	Sequence 3697, Ap
60	13.6	400	2	US-08-781-986A-3711	Sequence 3711, Ap
60	13.6	400	2	US-08-781-986A-3716	Sequence 3716, Ap
60	13.6	400	2	US-08-781-986A-3758	Sequence 3758, Ap
60	13.6	400	2	US-08-781-986A-3810	Sequence 3810, Ap
60	13.6	400	2	US-08-781-986A-3820	Sequence 3820, Ap
60	13.6	400	2	US-08-781-986A-3821	Sequence 3821, Ap
60	13.6	400	2	US-08-781-986A-3832	Sequence 3832, Ap
60	13.6	400	2	US-08-781-986A-3885	Sequence 3885, Ap
60	13.6	400	2	US-08-781-986A-3922	Sequence 3922, Ap

## ALIGNMENTS

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 06:09:34 ; Search time 238.091 Seconds  
(without alignments)  
2967.635 Million cell updates/sec

Title: US-10-600-642A-2

Perfect score: 442

Sequence: 1 gaagtcgtacaagtagcc.....agcggtatggaagttaa 442

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications\_NA\_New.\*
- 1: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
  - 2: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
  - 3: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
  - 4: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
  - 5: /EMC\_Celerra\_SID33/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
  - 6: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
  - 7: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
  - 8: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
  - 9: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
  - 10: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	60	13.6	4294	9	US-11-021-837-14
2	60	13.6	26683	9	US-11-021-837-26
3	52.8	11.9	1554	9	US-11-348-413-10825
4	52.4	11.9	1000	8	US-11-266-748A-206971
5	52.2	11.8	1000	8	US-11-266-748A-206292
6	46.8	10.6	1950	6	US-10-449-902-2950
7	46.6	10.5	1538	9	US-11-348-413-12
8	44.6	10.1	1452	6	US-10-511-345A-1
9	44.6	10.1	1531	8	US-11-256-221-1
10	42.6	9.6	902	8	US-11-266-748A-44347
11	42.6	9.6	274050	6	US-10-550-787-5
12	41.8	9.5	704	8	US-11-266-748A-195038
13	41.4	9.4	1526	9	US-11-350-955-4
14	41.4	9.4	1526	9	US-11-350-796-4
15	41.4	9.4	1528	9	US-11-350-955-2
16	41.4	9.4	1528	9	US-11-350-796-2
17	41.4	9.4	1529	9	US-11-350-955-3
18	41.4	9.4	1529	9	US-11-350-796-3
19	41.4	9.4	1532	9	US-11-350-955-1
20	41.4	9.4	1532	9	US-11-350-796-1
21	41	9.3	1542	8	US-11-331-987-3
22	39.2	8.9	5849	8	US-11-270-287-1
23	38.8	8.8	5155	8	US-11-266-748A-28283

## ALIGNMENTS

C	24	38.4	8.7	2718	9	US-11-218-305-12773	Sequence 12773, A
C	25	38.2	8.6	5976	6	US-10-517-441-554	Sequence 554, App
C	26	38	8.6	771	8	US-11-266-748A-41252	Sequence 41252, A
C	27	38	8.6	5493	6	US-10-517-441-417	Sequence 417, App
C	28	37.8	8.6	6001	6	US-10-517-441-777	Sequence 777, App
C	29	37.6	8.5	1142	8	US-11-216-545-1530	Sequence 1530, Ap
C	30	37.6	8.5	4009	9	US-11-218-305-3660	Sequence 3660, Ap
C	31	37.2	8.4	1826	8	US-11-216-545-774	Sequence 774, App
C	32	37	8.4	1175	9	US-11-218-305-18377	Sequence 18377, A
C	33	37	8.4	1602	6	US-10-449-902-11377	Sequence 11377, A
C	34	36.8	8.3	1399	8	US-11-266-748A-180787	Sequence 180787, A
C	35	36.8	8.3	1399	8	US-11-266-748A-241095	Sequence 241095, A
C	36	36.8	8.3	1581	9	US-11-056-358B-23650	Sequence 23650, A
C	37	36.6	8.3	896	8	US-11-266-748A-49860	Sequence 49860, A
C	38	36.6	8.3	1000	8	US-11-266-748A-285975	Sequence 285975, A
C	39	36.6	8.3	1000	8	US-11-266-748A-290882	Sequence 290882, A
C	40	36.6	8.3	1000	8	US-11-266-748A-337404	Sequence 337404, A
C	41	36.6	8.3	1000	8	US-11-266-748A-342311	Sequence 342311, A
C	42	36.6	8.3	1000	8	US-11-266-748A-402246	Sequence 402246, A
C	43	36.6	8.3	1000	8	US-11-266-748A-473292	Sequence 473292, A
C	44	36.6	8.3	2110	8	US-11-266-748A-30715	Sequence 30715, A
C	45	36.6	8.3	2153	8	US-11-266-748A-187554	Sequence 187554, A

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 05:46:51 ; Search time 5077.3 Seconds  
(without alignments)  
4868.007 Million cell updates/sec

Title: US-10-600-642A-2  
Perfect score: 442  
Sequence: 1 Gaagtcgtacaagtagcc.....agcggtatggaagttaa 442

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est3:\*

3: gb\_est4:\*

4: gb\_est5:\*

5: gb\_est6:\*

6: gb\_est7:\*

7: gb\_est8:\*

8: gb\_est9:\*

9: gb\_est10:\*

10: gb\_est11:\*

11: gb\_est12:\*

12: gb\_est13:\*

13: gb\_est14:\*

14: gb\_est15:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	61.8	14.0	371	13	CZ191241
C 2	61.8	14.0	809	13	CZ191243
C 3	60.8	13.8	6499	11	BH771024
C 4	59	13.3	390	5	CK339707
C 5	57.6	13.0	868	11	BH814965
C 6	57.6	13.0	1143	11	BH814966
C 7	57.4	13.0	723	9	DN616068
C 8	57.4	13.0	970	14	DU740944
C 9	56.4	12.8	781	13	CL680069
C 10	56.4	12.8	926	14	DU776044
C 11	56.2	12.7	967	14	DU750621
C 12	55.8	12.6	798	9	CX648081
C 13	55.2	12.5	364	9	DN255127
C 14	54.4	12.3	920	14	DU753933
C 15	54.2	12.3	805	14	DX079498
C 16	53.8	12.2	715	9	DN256273
C 17	53.6	12.1	870	14	DU769019
C 18	53.6	12.1	894	14	DU768642
C 19	53.6	12.1	905	14	DU733926

20	53.2	12.0	549	5	C1175518
21	52.8	11.9	1856	10	DV782961
22	52.6	11.9	307	11	BH675535
23	52.6	11.9	572	11	BH440331
24	52.6	11.9	631	11	BH861078
25	52.6	11.9	635	11	BH861097
26	52.6	11.9	666	11	BH442635
27	52.6	11.9	670	5	CD211293
28	52.6	11.9	671	11	BH572139
29	52.6	11.9	717	11	BH559104
30	52.6	11.9	736	11	BH732230
31	52.6	11.9	757	11	BZ441299
32	52.6	11.9	783	11	BH433849
33	52.6	11.9	801	11	BH556768
34	52.6	11.9	810	12	CC123417
35	52.6	11.9	812	11	BH431271
36	52.6	11.9	814	11	BZ425868
37	52.6	11.9	837	11	BZ520384
38	52.4	11.9	831	14	CT317837
39	52.2	11.8	351	8	CN028875
40	52.2	11.8	374	8	CN027713
41	52.2	11.8	380	8	CN027797
42	52.2	11.8	380	13	CW075218
43	52.2	11.8	500	9	DN257224
44	52.2	11.8	1571	12	CL066123
45	51.8	11.7	687	11	BZ429618

## ALIGNMENTS

C1175518	C1175518
DV782961	Hw_liver
BH675535	BOHTL47TF
BH440331	BOGGP28TF
BH861078	S14H6SP6
BH861097	B1E12T7 W
BH442635	BOGGA26TF
CD211293	H51_59 H0
BH572139	BOGXR35TR
BH559104	BOGZW82TR
BH732230	BOMMY63TF
BZ441299	BONMN23TR
BH433849	BOGUR44TR
BH556768	BOGLJ11TR
CC123417	NDL.73C23
BH431271	BOGKJ34TF
BZ425868	BONCH59TF
BZ520384	BOMOO15TF
CT317837	Sus scrofa
CN028875	UMC-pbliv
CN027713	UMC-p4civ
CN027797	UMC-p4civ
CW075218	104_356_1
DN257224	Meso09924
CL066123	CH216-107
BZ429618	BONLU78TR

## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.



GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:23:52 ; Search time 0.001 Seconds  
 (without alignments)  
 1583.244 Million cell updates/sec

Title: US-10-600-642A-2-COPY  
 Perfect score: 442  
 Sequence: 1 gaagtcgtaacaaggtagcc.....agcggttatggaaagtttaa 442

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 0.5

Searched: 21 seqs, 1791 residues

Total number of hits satisfying chosen parameters: 42

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 21 summaries

Database : gedb2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				
No.	Score	Query	Match	Length	DB	ID	Description
	1	442	100.0	442	1	E54412	ACCESSION:E54412
	2	442	100.0	442	1	AR408839	ACCESSION:AR408839
	3	442	100.0	442	1	AB022064	ACCESSION:AB022064
	4	50.4	11.4	52	1	BACRRDA	ACCESSION:M13610
	5	45.2	10.2	50	1	STMRR16S	ACCESSION:M26120
	6	26.8	6.1	30	1	CS001459	ACCESSION:CS001459
c	7	23.8	5.4	27	1	AR124123	ACCESSION:AR124123
c	8	23.8	5.4	27	1	AR282388	ACCESSION:AR282388
c	9	22	5.0	22	1	CQ880246	ACCESSION:CQ880246
c	10	22	5.0	22	1	CQ945361	ACCESSION:CQ945361
c	11	22	5.0	22	1	E10212	ACCESSION:E10212
c	12	21.6	4.9	22	1	AR147479	ACCESSION:AR147479
c	13	21.6	4.9	22	1	BD078568	ACCESSION:BD078568
c	14	21.6	4.9	22	1	AX076870	ACCESSION:AX076870
c	15	21	4.8	21	1	BD140325	ACCESSION:BD140325
c	16	21	4.8	21	1	CQ889258	ACCESSION:CQ889258
c	17	20.6	4.7	21	1	BD078551	ACCESSION:BD078551

C	18	20.6	4.7	21	1	BD167392
C	19	20.6	4.7	21	1	BD170790
C	20	20.6	4.7	21	1	AR234471
C	21	20.6	4.7	21	1	I57963

ACCESSION:BD167392
ACCESSION:BD170790
ACCESSION:AR234471
ACCESSION:I57963

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:06:04 ; Search time 1 Seconds  
(without alignments)  
7.619 Million cell updates/sec

Title: US-10-600-642A-1-COPY  
Perfect score: 624  
Sequence: 1 gaagtcgtaacaaggtagcc.....agcggttatggaaagttaa 624

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 239 seqs, 6105 residues

Total number of hits satisfying chosen parameters: 478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 239 summaries

Database : pubnewdb:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	70.6	11.3	77	1 US-11-348-413-10826	Sequence 10826, A
2	57.4	9.2	77	1 US-11-348-413-18	Sequence 18, Appl
3	55.2	8.8	76	1 US-11-348-413-10833	Sequence 10833, A
4	25	4.0	25	1 US-11-348-413-605683	Sequence 605683,
5	25	4.0	25	1 US-11-348-413-988264	Sequence 988264,
6	25	4.0	25	1 US-11-348-413-988265	Sequence 988265,
7	25	4.0	25	1 US-11-348-413-988266	Sequence 988266,
8	25	4.0	25	1 US-11-348-413-988267	Sequence 988267,
9	25	4.0	25	1 US-11-348-413-988268	Sequence 988268,
10	25	4.0	25	1 US-11-348-413-988269	Sequence 988269,
11	25	4.0	25	1 US-11-348-413-988270	Sequence 988270,
12	25	4.0	25	1 US-11-348-413-988271	Sequence 988271,
13	25	4.0	25	1 US-11-348-413-988272	Sequence 988272,
14	25	4.0	25	1 US-11-348-413-988273	Sequence 988273,
15	25	4.0	25	1 US-11-348-413-988274	Sequence 988274,
16	25	4.0	25	1 US-11-348-413-988275	Sequence 988275,
17	25	4.0	25	1 US-11-348-413-988276	Sequence 988276,
18	25	4.0	25	1 US-11-348-413-988277	Sequence 988277,

	19	25	4.0	25	1	US-11-348-413-988278	Sequence 988278,
	20	25	4.0	25	1	US-11-348-413-988279	Sequence 988279,
	21	25	4.0	25	1	US-11-348-413-988280	Sequence 988280,
	22	25	4.0	25	1	US-11-348-413-988281	Sequence 988281,
	23	25	4.0	25	1	US-11-348-413-988282	Sequence 988282,
	24	25	4.0	25	1	US-11-348-413-988283	Sequence 988283,
	25	25	4.0	25	1	US-11-348-413-988284	Sequence 988284,
	26	24	3.8	25	1	US-11-348-413-988285	Sequence 988285,
	27	23.4	3.7	25	1	US-11-348-413-605858	Sequence 605858,
	28	23.4	3.7	25	1	US-11-348-413-605859	Sequence 605859,
	29	23.4	3.7	25	1	US-11-348-413-988286	Sequence 988286,
c	30	23.4	3.7	25	1	US-11-348-413-1073654	Sequence 1073654,
c	31	23.4	3.7	25	1	US-11-348-413-1073655	Sequence 1073655,
	32	22.4	3.6	25	1	US-11-348-413-605387	Sequence 605387,
	33	22.4	3.6	25	1	US-11-348-413-605860	Sequence 605860,
	34	22.4	3.6	25	1	US-11-348-413-988811	Sequence 988811,
c	35	22	3.5	28	1	US-11-401-826-7	Sequence 7, Appli
c	36	22	3.5	28	1	US-11-255-290-7	Sequence 7, Appli
	37	21.8	3.5	25	1	US-11-348-413-605358	Sequence 605358,
	38	21.8	3.5	25	1	US-11-348-413-605359	Sequence 605359,
	39	21.8	3.5	25	1	US-11-348-413-605360	Sequence 605360,
	40	21.8	3.5	25	1	US-11-348-413-605388	Sequence 605388,
	41	21.8	3.5	25	1	US-11-348-413-605389	Sequence 605389,
	42	21.8	3.5	25	1	US-11-348-413-605390	Sequence 605390,
	43	21.8	3.5	25	1	US-11-348-413-605391	Sequence 605391,
	44	21.8	3.5	25	1	US-11-348-413-605392	Sequence 605392,
	45	21.8	3.5	25	1	US-11-348-413-605393	Sequence 605393,
	46	21.8	3.5	25	1	US-11-348-413-605394	Sequence 605394,
	47	21.8	3.5	25	1	US-11-348-413-605861	Sequence 605861,
	48	21.8	3.5	25	1	US-11-348-413-605862	Sequence 605862,
	49	21.8	3.5	25	1	US-11-348-413-605863	Sequence 605863,
	50	21.8	3.5	25	1	US-11-348-413-605864	Sequence 605864,
	51	21.8	3.5	25	1	US-11-348-413-988287	Sequence 988287,
	52	21.8	3.5	25	1	US-11-348-413-988288	Sequence 988288,
	53	21.8	3.5	25	1	US-11-348-413-988289	Sequence 988289,
	54	21.8	3.5	25	1	US-11-348-413-988290	Sequence 988290,
	55	21.8	3.5	25	1	US-11-348-413-988526	Sequence 988526,
	56	21.8	3.5	25	1	US-11-348-413-988527	Sequence 988527,
	57	21.8	3.5	25	1	US-11-348-413-988528	Sequence 988528,
	58	21.8	3.5	25	1	US-11-348-413-988812	Sequence 988812,
	59	21.8	3.5	25	1	US-11-348-413-988813	Sequence 988813,
	60	21.8	3.5	25	1	US-11-348-413-988814	Sequence 988814,
	61	21.8	3.5	25	1	US-11-348-413-988815	Sequence 988815,
	62	21.8	3.5	25	1	US-11-348-413-988816	Sequence 988816,
	63	21.8	3.5	25	1	US-11-348-413-988817	Sequence 988817,
	64	21.8	3.5	25	1	US-11-348-413-988818	Sequence 988818,
c	65	21.8	3.5	25	1	US-11-348-413-1073651	Sequence 1073651,
c	66	21.8	3.5	25	1	US-11-348-413-1073652	Sequence 1073652,
c	67	21.8	3.5	25	1	US-11-348-413-1073653	Sequence 1073653,
c	68	21.6	3.5	22	1	US-11-265-833-2	Sequence 2, Appli
c	69	21.4	3.4	25	1	US-11-348-413-1073656	Sequence 1073656,
c	70	21.2	3.4	27	1	US-11-368-333-6	Sequence 6, Appli
	71	20.8	3.3	25	1	US-11-348-413-605361	Sequence 605361,
	72	20.8	3.3	25	1	US-11-348-413-605395	Sequence 605395,
	73	20.8	3.3	25	1	US-11-348-413-605865	Sequence 605865,
	74	20.8	3.3	25	1	US-11-348-413-988291	Sequence 988291,
	75	20.8	3.3	25	1	US-11-348-413-988303	Sequence 988303,

	76	20.8	3.3	25	1	US-11-348-413-988529	Sequence 988529,
	77	20.8	3.3	25	1	US-11-348-413-988819	Sequence 988819,
	78	20.8	3.3	25	1	US-11-348-413-1222109	Sequence 1222109,
	79	20.8	3.3	25	1	US-11-348-413-1222110	Sequence 1222110,
	80	20.2	3.2	25	1	US-11-348-413-197726	Sequence 197726,
	81	20.2	3.2	25	1	US-11-348-413-557383	Sequence 557383,
	82	20.2	3.2	25	1	US-11-348-413-605362	Sequence 605362,
	83	20.2	3.2	25	1	US-11-348-413-605363	Sequence 605363,
	84	20.2	3.2	25	1	US-11-348-413-605364	Sequence 605364,
	85	20.2	3.2	25	1	US-11-348-413-605365	Sequence 605365,
	86	20.2	3.2	25	1	US-11-348-413-605366	Sequence 605366,
	87	20.2	3.2	25	1	US-11-348-413-605396	Sequence 605396,
	88	20.2	3.2	25	1	US-11-348-413-605397	Sequence 605397,
	89	20.2	3.2	25	1	US-11-348-413-605398	Sequence 605398,
	90	20.2	3.2	25	1	US-11-348-413-605399	Sequence 605399,
	91	20.2	3.2	25	1	US-11-348-413-605400	Sequence 605400,
	92	20.2	3.2	25	1	US-11-348-413-605401	Sequence 605401,
	93	20.2	3.2	25	1	US-11-348-413-605402	Sequence 605402,
	94	20.2	3.2	25	1	US-11-348-413-605866	Sequence 605866,
	95	20.2	3.2	25	1	US-11-348-413-605867	Sequence 605867,
	96	20.2	3.2	25	1	US-11-348-413-605868	Sequence 605868,
	97	20.2	3.2	25	1	US-11-348-413-605869	Sequence 605869,
	98	20.2	3.2	25	1	US-11-348-413-808694	Sequence 808694,
	99	20.2	3.2	25	1	US-11-348-413-808695	Sequence 808695,
	100	20.2	3.2	25	1	US-11-348-413-808697	Sequence 808697,
	101	20.2	3.2	25	1	US-11-348-413-988292	Sequence 988292,
	102	20.2	3.2	25	1	US-11-348-413-988293	Sequence 988293,
	103	20.2	3.2	25	1	US-11-348-413-988301	Sequence 988301,
	104	20.2	3.2	25	1	US-11-348-413-988302	Sequence 988302,
	105	20.2	3.2	25	1	US-11-348-413-988530	Sequence 988530,
	106	20.2	3.2	25	1	US-11-348-413-988531	Sequence 988531,
	107	20.2	3.2	25	1	US-11-348-413-988532	Sequence 988532,
	108	20.2	3.2	25	1	US-11-348-413-988820	Sequence 988820,
	109	20.2	3.2	25	1	US-11-348-413-988821	Sequence 988821,
	110	20.2	3.2	25	1	US-11-348-413-988822	Sequence 988822,
	111	20.2	3.2	25	1	US-11-348-413-988823	Sequence 988823,
	112	20.2	3.2	25	1	US-11-348-413-988824	Sequence 988824,
c	113	20.2	3.2	25	1	US-11-348-413-1073649	Sequence 1073649,
c	114	20.2	3.2	25	1	US-11-348-413-1073650	Sequence 1073650,
	115	20.2	3.2	25	1	US-11-348-413-1222108	Sequence 1222108,
	116	20.2	3.2	25	1	US-11-348-413-1222134	Sequence 1222134,
	117	20.2	3.2	25	1	US-11-348-413-1222135	Sequence 1222135,
c	118	20	3.2	20	1	US-10-510-329-13	Sequence 13, Appl
c	119	20	3.2	20	1	US-11-324-675-2	Sequence 2, Appli
	120	19.8	3.2	25	1	US-11-348-413-605403	Sequence 605403,
	121	19.8	3.2	25	1	US-11-348-413-605404	Sequence 605404,
	122	19.8	3.2	25	1	US-11-348-413-808696	Sequence 808696,
	123	19.8	3.2	25	1	US-11-348-413-1222111	Sequence 1222111,
	124	19.8	3.2	25	1	US-11-348-413-1222136	Sequence 1222136,
c	125	19.4	3.1	25	1	US-11-348-413-1073657	Sequence 1073657,
	126	19.2	3.1	25	1	US-11-348-413-605367	Sequence 605367,
	127	19.2	3.1	25	1	US-11-348-413-605373	Sequence 605373,
	128	19.2	3.1	25	1	US-11-348-413-605374	Sequence 605374,
	129	19.2	3.1	25	1	US-11-348-413-605870	Sequence 605870,
	130	19.2	3.1	25	1	US-11-348-413-808677	Sequence 808677,
	131	19.2	3.1	25	1	US-11-348-413-808678	Sequence 808678,
	132	19.2	3.1	25	1	US-11-348-413-808698	Sequence 808698,

133	19.2	3.1	25	1	US-11-348-413-808699	Sequence 808699,
134	19.2	3.1	25	1	US-11-348-413-808700	Sequence 808700,
135	19.2	3.1	25	1	US-11-348-413-988294	Sequence 988294,
136	19.2	3.1	25	1	US-11-348-413-988300	Sequence 988300,
137	19.2	3.1	25	1	US-11-348-413-988533	Sequence 988533,
138	19.2	3.1	25	1	US-11-348-413-988539	Sequence 988539,
139	19.2	3.1	25	1	US-11-348-413-988540	Sequence 988540,
140	19.2	3.1	25	1	US-11-348-413-988825	Sequence 988825,
141	19.2	3.1	25	1	US-11-348-413-1222107	Sequence 1222107,
142	19.2	3.1	25	1	US-11-348-413-1222138	Sequence 1222138,
c 143	19	3.0	19	1	US-11-373-989-2	Sequence 2, Appli
144	18.8	3.0	25	1	US-11-348-413-605405	Sequence 605405,
145	18.8	3.0	25	1	US-11-348-413-808673	Sequence 808673,
146	18.8	3.0	25	1	US-11-348-413-808674	Sequence 808674,
147	18.8	3.0	25	1	US-11-348-413-808675	Sequence 808675,
148	18.8	3.0	25	1	US-11-348-413-808676	Sequence 808676,
c 149	18.8	3.0	25	1	US-11-348-413-864463	Sequence 864463,
c 150	18.8	3.0	25	1	US-11-348-413-864464	Sequence 864464,
c 151	18.8	3.0	25	1	US-11-348-413-864465	Sequence 864465,
152	18.8	3.0	25	1	US-11-348-413-972194	Sequence 972194,
153	18.8	3.0	25	1	US-11-348-413-1009479	Sequence 1009479,
154	18.8	3.0	25	1	US-11-348-413-1222105	Sequence 1222105,
155	18.8	3.0	25	1	US-11-348-413-1222106	Sequence 1222106,
156	18.8	3.0	25	1	US-11-348-413-1222112	Sequence 1222112,
157	18.6	3.0	25	1	US-11-348-413-605368	Sequence 605368,
158	18.6	3.0	25	1	US-11-348-413-605369	Sequence 605369,
159	18.6	3.0	25	1	US-11-348-413-605370	Sequence 605370,
160	18.6	3.0	25	1	US-11-348-413-605371	Sequence 605371,
161	18.6	3.0	25	1	US-11-348-413-605372	Sequence 605372,
162	18.6	3.0	25	1	US-11-348-413-605406	Sequence 605406,
163	18.6	3.0	25	1	US-11-348-413-605407	Sequence 605407,
164	18.6	3.0	25	1	US-11-348-413-605408	Sequence 605408,
165	18.6	3.0	25	1	US-11-348-413-605857	Sequence 605857,
166	18.6	3.0	25	1	US-11-348-413-605871	Sequence 605871,
167	18.6	3.0	25	1	US-11-348-413-605872	Sequence 605872,
168	18.6	3.0	25	1	US-11-348-413-605873	Sequence 605873,
169	18.6	3.0	25	1	US-11-348-413-808065	Sequence 808065,
170	18.6	3.0	25	1	US-11-348-413-808066	Sequence 808066,
171	18.6	3.0	25	1	US-11-348-413-808067	Sequence 808067,
172	18.6	3.0	25	1	US-11-348-413-808068	Sequence 808068,
173	18.6	3.0	25	1	US-11-348-413-808701	Sequence 808701,
174	18.6	3.0	25	1	US-11-348-413-808702	Sequence 808702,
c 175	18.6	3.0	25	1	US-11-348-413-864460	Sequence 864460,
c 176	18.6	3.0	25	1	US-11-348-413-864461	Sequence 864461,
c 177	18.6	3.0	25	1	US-11-348-413-864466	Sequence 864466,
178	18.6	3.0	25	1	US-11-348-413-988295	Sequence 988295,
179	18.6	3.0	25	1	US-11-348-413-988296	Sequence 988296,
180	18.6	3.0	25	1	US-11-348-413-988297	Sequence 988297,
181	18.6	3.0	25	1	US-11-348-413-988298	Sequence 988298,
182	18.6	3.0	25	1	US-11-348-413-988299	Sequence 988299,
183	18.6	3.0	25	1	US-11-348-413-988489	Sequence 988489,
184	18.6	3.0	25	1	US-11-348-413-988534	Sequence 988534,
185	18.6	3.0	25	1	US-11-348-413-988535	Sequence 988535,
186	18.6	3.0	25	1	US-11-348-413-988536	Sequence 988536,
187	18.6	3.0	25	1	US-11-348-413-988537	Sequence 988537,
188	18.6	3.0	25	1	US-11-348-413-988538	Sequence 988538,
189	18.6	3.0	25	1	US-11-348-413-988826	Sequence 988826,

	190	18.6	3.0	25	1	US-11-348-413-1064914	Sequence 1064914,
c	191	18.6	3.0	25	1	US-11-348-413-1165354	Sequence 1165354,
	192	18.6	3.0	25	1	US-11-348-413-1210461	Sequence 1210461,
	193	18.6	3.0	25	1	US-11-348-413-1210462	Sequence 1210462,
	194	18.6	3.0	25	1	US-11-348-413-1222137	Sequence 1222137,
	195	18.6	3.0	25	1	US-11-348-413-1222139	Sequence 1222139,
	196	18.6	3.0	25	1	US-11-348-413-1222140	Sequence 1222140,
	197	18.4	2.9	25	1	US-11-348-413-808064	Sequence 808064,
c	198	18.4	2.9	25	1	US-11-348-413-864462	Sequence 864462,
	199	18.2	2.9	25	1	US-11-217-529-118810	Sequence 118810,
c	200	18.2	2.9	25	1	US-11-348-413-202363	Sequence 202363,
	201	18.2	2.9	25	1	US-11-348-413-605375	Sequence 605375,
	202	18.2	2.9	25	1	US-11-348-413-808679	Sequence 808679,
	203	18.2	2.9	25	1	US-11-348-413-988541	Sequence 988541,
	204	18.2	2.9	25	1	US-11-348-413-988827	Sequence 988827,
	205	18.2	2.9	25	1	US-11-348-413-988828	Sequence 988828,
	206	18.2	2.9	25	1	US-11-348-413-1055941	Sequence 1055941,
c	207	18.2	2.9	25	1	US-11-348-413-1073648	Sequence 1073648,
c	208	18	2.9	18	1	US-11-350-955-9	Sequence 9, Appli
c	209	18	2.9	18	1	US-11-350-796-9	Sequence 9, Appli
	210	17.8	2.9	25	1	US-11-348-413-797854	Sequence 797854,
c	211	17.8	2.9	25	1	US-11-348-413-804342	Sequence 804342,
	212	17.8	2.9	25	1	US-11-348-413-808672	Sequence 808672,
c	213	17.8	2.9	25	1	US-11-348-413-1009551	Sequence 1009551,
	214	17.8	2.9	25	1	US-11-348-413-1222104	Sequence 1222104,
	215	17.8	2.9	25	1	US-11-348-413-1222113	Sequence 1222113,
c	216	17.6	2.8	25	1	US-11-348-413-222739	Sequence 222739,
	217	17.6	2.8	25	1	US-11-348-413-350696	Sequence 350696,
	218	17.6	2.8	25	1	US-11-348-413-434686	Sequence 434686,
	219	17.6	2.8	25	1	US-11-348-413-434687	Sequence 434687,
	220	17.6	2.8	25	1	US-11-348-413-572608	Sequence 572608,
	221	17.6	2.8	25	1	US-11-348-413-605379	Sequence 605379,
	222	17.6	2.8	25	1	US-11-348-413-605380	Sequence 605380,
	223	17.6	2.8	25	1	US-11-348-413-605409	Sequence 605409,
	224	17.6	2.8	25	1	US-11-348-413-605874	Sequence 605874,
	225	17.6	2.8	25	1	US-11-348-413-808069	Sequence 808069,
	226	17.6	2.8	25	1	US-11-348-413-808703	Sequence 808703,
	227	17.6	2.8	25	1	US-11-348-413-808707	Sequence 808707,
	228	17.6	2.8	25	1	US-11-348-413-808708	Sequence 808708,
c	229	17.6	2.8	25	1	US-11-348-413-864459	Sequence 864459,
c	230	17.6	2.8	25	1	US-11-348-413-864467	Sequence 864467,
c	231	17.6	2.8	25	1	US-11-348-413-900967	Sequence 900967,
	232	17.6	2.8	25	1	US-11-348-413-930121	Sequence 930121,
	233	17.6	2.8	25	1	US-11-348-413-988488	Sequence 988488,
	234	17.6	2.8	25	1	US-11-348-413-988490	Sequence 988490,
	235	17.6	2.8	25	1	US-11-348-413-988545	Sequence 988545,
	236	17.6	2.8	25	1	US-11-348-413-988546	Sequence 988546,
	237	17.6	2.8	25	1	US-11-348-413-1075989	Sequence 1075989,
	238	17.6	2.8	25	1	US-11-348-413-1222141	Sequence 1222141,
	239	17.6	2.8	25	1	US-11-348-413-1238534	Sequence 1238534,

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:27:10 ; Search time 0.001 Seconds  
 (without alignments)  
 896.376 Million cell updates/sec

Title: US-10-600-642A-2-COPY  
 Perfect score: 442  
 Sequence: 1 gaagtcgtaacaaggtagcc.....agcggttatggaaagttaa 442

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 0.5

Searched: 24 seqs, 1014 residues

Total number of hits satisfying chosen parameters: 48

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 24 summaries

Database : pubmaindb2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	442	100.0	442	1	US-10-600-642-2	Sequence 2, Appli	
2	26.8	6.1	30	1	US-10-881-813-4	Sequence 4, Appli	
3	26	5.9	35	1	US-10-223-126-202	Sequence 202, App	
4	26	5.9	35	1	US-11-070-519-202	Sequence 202, App	
5	25.2	5.7	30	1	US-10-831-286A-16801	Sequence 16801, A	
6	25	5.7	25	1	US-10-401-343-42	Sequence 42, Appl	
7	25	5.7	25	1	US-11-237-807-42	Sequence 42, Appl	
8	23.6	5.3	30	1	US-09-807-723-1	Sequence 1, Appli	
9	23.6	5.3	30	1	US-10-770-183-1	Sequence 1, Appli	
c 10	22	5.0	22	1	US-09-991-518A-2	Sequence 2, Appli	
c 11	22	5.0	22	1	US-10-810-550-110	Sequence 110, App	
c 12	22	5.0	22	1	US-10-805-292-76	Sequence 76, Appl	
c 13	22	5.0	22	1	US-10-972-530-10	Sequence 10, Appl	
c 14	22	5.0	22	1	US-10-848-126-76	Sequence 76, Appl	
c 15	22	5.0	22	1	US-11-228-416-2	Sequence 2, Appli	
c 16	21.6	4.9	22	1	US-10-396-446-5	Sequence 5, Appli	
c 17	21.6	4.9	22	1	US-10-477-469-10	Sequence 10, Appl	



c	18	21.6	4.9	22	1	US-11-273-617-13	Sequence 13, Appl
	19	21.4	4.8	23	1	US-10-360-935-37	Sequence 37, Appl
c	20	21.2	4.8	27	1	US-10-407-952-6	Sequence 6, Appli
	21	21	4.8	21	1	US-10-438-774-5	Sequence 5, Appli
c	22	20.6	4.7	21	1	US-10-212-476-4	Sequence 4, Appli
c	23	20.6	4.7	21	1	US-10-466-016-2	Sequence 2, Appli
c	24	20.6	4.7	21	1	US-10-793-643A-2	Sequence 2, Appli

OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:04:59 ; Search time 0.001 Seconds  
 (without alignments)  
 2875.392 Million cell updates/sec

Title: US-10-600-642A-1-COPY  
 Perfect score: 624  
 Sequence: 1 gaagtcgtaacaaggttagcc.....agcggttatggaaagttaa 624

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 0.5

Searched: 22 seqs, 2304 residues

Total number of hits satisfying chosen parameters: 44

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 22 summaries

Database : pubmaindb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	624	100.0	624	1	US-10-600-642-1	Sequence 1, Appli
2	337.8	54.1	442	1	US-10-600-642-2	Sequence 2, Appli
3	69	11.1	77	1	US-09-974-300-8397	Sequence 8397, Ap
4	69	11.1	77	1	US-09-974-300-8406	Sequence 8406, Ap
5	69	11.1	77	1	US-09-974-300-8454	Sequence 8454, Ap
6	67.6	10.8	74	1	US-10-857-625-228	Sequence 228, App
7	67.6	10.8	74	1	US-10-857-625-388	Sequence 388, App
8	67.4	10.8	77	1	US-09-974-300-4362	Sequence 4362, Ap
9	67.4	10.8	77	1	US-09-974-300-4371	Sequence 4371, Ap
10	67.4	10.8	77	1	US-09-974-300-4377	Sequence 4377, Ap
11	67.4	10.8	77	1	US-09-974-300-4419	Sequence 4419, Ap
12	66.4	10.6	76	1	US-09-974-300-4375	Sequence 4375, Ap
13	66.4	10.6	76	1	US-09-974-300-4436	Sequence 4436, Ap
14	52.2	8.4	73	1	US-10-857-625-226	Sequence 226, App
15	52.2	8.4	73	1	US-10-857-625-389	Sequence 389, App
16	52.2	8.4	73	1	US-10-857-625-400	Sequence 400, App
17	26.8	4.3	30	1	US-10-881-813-4	Sequence 4, Appli

18	26	4.2	35	1	US-10-223-126-202	Sequence 202, App
19	26	4.2	35	1	US-11-070-519-202	Sequence 202, App
20	25.2	4.0	30	1	US-10-831-286A-16801	Sequence 16801, A
21	25	4.0	25	1	US-10-401-343-42	Sequence 42, Appl
22	25	4.0	25	1	US-11-237-807-42	Sequence 42, Appl

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:07:10 ; Search time 0.001 Seconds  
(without alignments)  
5257.824 Million cell updates/sec

Title: US-10-600-642A-1-COPY  
Perfect score: 624  
Sequence: 1 gaagtcgtaacaaggtagcc.....agcggttatggaaagttaa 624

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 22 seqs, 4213 residues

Total number of hits satisfying chosen parameters: 44

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 22 summaries

Database : gedb:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	624	100.0	624	1	E54411	ACCESSION:E54411
2	624	100.0	624	1	AR408838	ACCESSION:AR408838
3	624	100.0	624	1	AB022063	ACCESSION:AB022063
4	337.8	54.1	442	1	E54412	ACCESSION:E54412
5	337.8	54.1	442	1	AR408839	ACCESSION:AR408839
6	337.8	54.1	442	1	AB022064	ACCESSION:AB022064
7	69	11.1	77	1	AX439982	ACCESSION:AX439982
8	69	11.1	77	1	AX439991	ACCESSION:AX439991
9	69	11.1	77	1	AX440039	ACCESSION:AX440039
10	67.4	10.8	77	1	AX435947	ACCESSION:AX435947
11	67.4	10.8	77	1	AX435956	ACCESSION:AX435956
12	67.4	10.8	77	1	AX435962	ACCESSION:AX435962
13	67.4	10.8	77	1	AX436004	ACCESSION:AX436004
14	66.4	10.6	76	1	AX435960	ACCESSION:AX435960
15	66.4	10.6	76	1	AX436021	ACCESSION:AX436021
16	60	9.6	77	1	ECOTRI1	ACCESSION:K00217
17	50.4	8.1	52	1	BACRRDA	ACCESSION:M13610
18	48.2	7.7	61	1	AB201400	ACCESSION:AB201400

	19	45.2	7.2	50	1	STMRR16S
	20	26.8	4.3	30	1	CS001459
c	21	23.8	3.8	27	1	AR124123
c	22	23.8	3.8	27	1	AR282388

ACCESSION:M26120  
ACCESSION:CS001459  
ACCESSION:AR124123  
ACCESSION:AR282388

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:02:08 ; Search time 1 Seconds  
(without alignments)  
2.621 Million cell updates/sec

Title: US-10-600-642A-1-COPY  
Perfect score: 624  
Sequence: 1 gaagtcgtaacaaggtagcc.....agcggttatggaaagttaa 624

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 27 seqs, 2100 residues

Total number of hits satisfying chosen parameters: 54

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 27 summaries

Database : issdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	624	100.0	624	1	US-09-762-633-1
2	337.8	54.1	442	1	US-09-762-633-2
3	69	11.1	77	1	US-09-974-300-8397
4	69	11.1	77	1	US-09-974-300-8406
5	69	11.1	77	1	US-09-974-300-8454
6	67.4	10.8	77	1	US-09-974-300-4362
7	67.4	10.8	77	1	US-09-974-300-4371
8	67.4	10.8	77	1	US-09-974-300-4377
9	67.4	10.8	77	1	US-09-974-300-4419
10	66.4	10.6	76	1	US-09-974-300-4375
11	66.4	10.6	76	1	US-09-974-300-4436
c 12	23.8	3.8	27	1	US-09-252-806-2
c 13	23.8	3.8	27	1	US-09-711-508-2
c 14	21.6	3.5	22	1	US-08-995-960-18
c 15	21.6	3.5	22	1	US-08-953-171-39
c 16	21.6	3.5	22	1	US-09-193-377B-61
c 17	20.6	3.3	21	1	US-08-266-414-3

Score / length  
seq 1

c	18	20.6	3.3	21	1	US-08-953-171-22	Sequence 22, Appl
c	19	20.6	3.3	21	1	US-09-261-115-4	Sequence 4, Appli
	20	20	3.2	20	1	US-08-445-289B-9	Sequence 9, Appli
c	21	20	3.2	20	1	US-09-073-465-17	Sequence 17, Appl
	22	20	3.2	20	1	US-09-398-179-5	Sequence 5, Appli
c	23	20	3.2	20	1	US-09-883-405-2	Sequence 2, Appli
c	24	20	3.2	20	1	US-10-085-871C-8	Sequence 8, Appli
c	25	20	3.2	20	1	US-10-085-871C-12	Sequence 12, Appl
c	26	20	3.2	20	1	US-09-856-221-5	Sequence 5, Appli
c	27	20	3.2	20	1	US-10-166-225A-3	Sequence 3, Appli

OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:03:40 ; Search time 0.001 Seconds  
 (without alignments)  
 5683.392 Million cell updates/sec

Title: US-10-600-642A-1-COPY  
 Perfect score: 624  
 Sequence: 1 gaagtcgtaacaaggtagcc.....agcggttatggaaagttaa 624

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 0.5

Searched: 74 seqs, 4554 residues

Total number of hits satisfying chosen parameters: 148

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 74 summaries

Database : ngsdb:\*

*score length genesca  
 SID 1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			%				Description
	No.	Score	Query Match	Length	DB	ID	
1	624	100.0	624	1	AAZ91771	Spacer region betw	
2	624	100.0	624	1	AAI71855	Pectinatus frising	
3	337.8	54.1	442	1	AAZ91772	Spacer region betw	
4	337.8	54.1	442	1	AAI71856	Pectinatus frising	
5	69	11.1	77	1	ABK81163	Bacillus clausii g	
6	69	11.1	77	1	ABK81115	Bacillus clausii g	
7	69	11.1	77	1	ABK81106	Bacillus clausii g	
8	67.6	10.8	74	1	ADW94448	Proliferation-requ	
9	67.6	10.8	74	1	ADW94288	Proliferation-requ	
10	67.4	10.8	77	1	ABK77071	Bacillus lichenifo	
11	67.4	10.8	77	1	ABK77080	Bacillus lichenifo	
12	67.4	10.8	77	1	ABK77128	Bacillus lichenifo	
13	67.4	10.8	77	1	ABK77086	Bacillus lichenifo	
14	66.4	10.6	76	1	ABK77145	Bacillus lichenifo	
15	66.4	10.6	76	1	ABK77084	Bacillus lichenifo	
16	52.2	8.4	73	1	ADW94460	Proliferation-requ	
17	52.2	8.4	73	1	ADW94286	Proliferation-requ	
18	52.2	8.4	73	1	ADW94449	Proliferation-requ	



	19	30.4	4.9	41	1	ADB61527	Prokaryotic gene s
	20	29.8	4.8	40	1	AEC64592	Organochlorine com
	21	28.8	4.6	40	1	AEC64617	Organochlorine com
	22	28.8	4.6	40	1	AEC64616	Organochlorine com
	23	26.8	4.3	30	1	ADX17032	Lemna minor chloro
c	24	26	4.2	26	1	AAQ92375	DNA primer. Synth
	25	26	4.2	35	1	ACC97191	Consensus 16S rRNA
	26	25	4.0	25	1	ADF69484	Tapesia acuformisI
c	27	23.8	3.8	27	1	AAX04478	Strain MO7 16S rDN
c	28	23.6	3.8	30	1	AAQ71864	Eucaryotic nuclear
	29	23.6	3.8	30	1	AAI64203	Primer 1P for the
c	30	23.4	3.7	25	1	AAQ44665	Primer #1 for PCR/
c	31	22.2	3.6	27	1	AAV21874	Antisense oligo NB
c	32	22.2	3.6	27	1	AAV17792	Microorganism MO7
c	33	22	3.5	22	1	AAX04638	PCR primer 2 used
c	34	22	3.5	22	1	AAZ09417	E. coli 16S rRNA s
	35	22	3.5	22	1	AAK99084	S. aureus 16S-rRNA
c	36	22	3.5	22	1	ABN84205	Salinospora sp. 16
	37	22	3.5	22	1	AAK99123	Staphylococcus aur
c	38	22	3.5	22	1	ADS18913	Reverse PCR primer
c	39	22	3.5	22	1	ADU40707	Novel nucleotide a
c	40	22	3.5	22	1	ADZ66121	16s rRNA reverse P
c	41	22	3.5	22	1	ADU76905	16s rRNA reverse P
c	42	22	3.5	22	1	ADZ69178	Eubacterial PCR pr
c	43	22	3.5	22	1	AEC81382	Dehalococcoides ba
c	44	22	3.5	22	1	AEF24204	rRNA SSU primer RC
c	45	21.6	3.5	22	1	AAX82007	Bacterial 16S rRNA
c	46	21.6	3.5	22	1	AAZ86877	16S rRNA PCR prime
c	47	21.6	3.5	22	1	AAF54840	Primer used for sp
c	48	21.6	3.5	22	1	ABZ69287	J lividum 16s ribo
c	49	21.6	3.5	22	1	ABZ23953	A. radiobacter 16S
c	50	21.6	3.5	22	1	ADG25781	Bacterial universa
c	51	21.6	3.5	22	1	ADK65756	Reverse primer 149
c	52	21.6	3.5	22	1	ADU39844	Alcanivorax sp. OK
c	53	21.6	3.5	22	1	ADV25289	Primer 1492R used
c	54	21.6	3.5	22	1	ADW16281	PCR primer 1492r t
	55	21.4	3.4	23	1	ADS17007	Primer used to det
c	56	21.2	3.4	27	1	ADE85928	Escherichia coli 1
c	57	21	3.4	21	1	AAQ10127	Probe 1640 to the
c	58	21	3.4	21	1	AAT11573	16S rRNA reverse p
c	59	21	3.4	21	1	AAV21120	16S rRNA Escherich
	60	21	3.4	21	1	AAH73860	Cyanophycean PCR p
c	61	21	3.4	21	1	ACC48610	Erwinia pyrifoliae
c	62	21	3.4	21	1	ADL15738	Bacillus CMB26 str
c	63	21	3.4	21	1	ADS75285	Universal PCR prim
c	64	21	3.4	21	1	AEC09675	Primer 16S-2, seq
c	65	21	3.4	21	1	AEE19758	Pseudomonas chloro
c	66	21	3.4	21	1	AEE75252	Acinetobacter sp.
	67	21	3.4	24	1	AAI69778	16S/23SrRNA spacer
c	68	20.6	3.3	21	1	AAT60344	Reverse primer for
c	69	20.6	3.3	21	1	AAV45917	Biosensor oligonuc
c	70	20.6	3.3	21	1	AAX57749	Oligonucleotide 14
c	71	20.6	3.3	21	1	AAC58781	Bacterial 16S rRNA
c	72	20.6	3.3	21	1	ABS53672	Antimicrobial agen
c	73	20.6	3.3	21	1	ADV96672	Rhizobium 16S rDNA
c	74	20.6	3.3	27	1	AAV21876	Nuclease resistant

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:25:09 ; Search time 0.001 Seconds  
(without alignments)  
2085.356 Million cell updates/sec

Title: US-10-600-642A-2-COPY  
Perfect score: 442  
Sequence: 1 gaagtcgtaacaaggtagcc.....agcggttatggaaagttaa 442

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 100 seqs, 2359 residues

Total number of hits satisfying chosen parameters: 200

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 101 summaries

Database : issdb2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No:	%		Query Match	Length	DB	ID	Description
	Score						
1	442	100.0	442	1	US-09-762-633-2	Sequence 2, Appli	
c 2	23.8	5.4	27	1	US-09-252-806-2	Sequence 2, Appli	
c 3	23.8	5.4	27	1	US-09-711-508-2	Sequence 2, Appli	
c 4	21.6	4.9	22	1	US-08-995-960-18	Sequence 18, Appl	
c 5	21.6	4.9	22	1	US-08-953-171-39	Sequence 39, Appl	
c 6	21.6	4.9	22	1	US-09-193-377B-61	Sequence 61, Appl	
c 7	20.6	4.7	21	1	US-08-266-414-3	Sequence 3, Appli	
c 8	20.6	4.7	21	1	US-08-953-171-22	Sequence 22, Appl	
c 9	20.6	4.7	21	1	US-09-261-115-4	Sequence 4, Appli	
10	20	4.5	20	1	US-08-445-289B-9	Sequence 9, Appli	
c 11	20	4.5	20	1	US-09-073-465-17	Sequence 17, Appl	
12	20	4.5	20	1	US-09-398-179-5	Sequence 5, Appli	
c 13	20	4.5	20	1	US-09-883-405-2	Sequence 2, Appli	
c 14	20	4.5	20	1	US-10-085-871C-8	Sequence 8, Appli	
c 15	20	4.5	20	1	US-10-085-871C-12	Sequence 12, Appl	
c 16	20	4.5	20	1	US-09-856-221-5	Sequence 5, Appli	
c 17	20	4.5	20	1	US-10-166-225A-3	Sequence 3, Appli	
c 18	19	4.3	19	1	US-09-924-097A-17	Sequence 17, Appl	

Score / length  
seq 2

c	19	19	4.3	19	1	US-09-762-633-5	Sequence 5, Appli
c	20	19	4.3	19	1	US-10-069-977-2	Sequence 2, Appli
c	21	19	4.3	19	1	US-10-069-977-5	Sequence 5, Appli
c	22	19	4.3	442	1	US-09-762-633-2	Sequence 2, Appli
c	23	18.6	4.2	19	1	US-09-557-248-4	Sequence 4, Appli
c	24	18.6	4.2	20	1	US-10-053-243-9	Sequence 9, Appli
	25	18.4	4.2	20	1	US-08-445-289B-7	Sequence 7, Appli
	26	18.4	4.2	20	1	US-08-445-289B-10	Sequence 10, Appl
c	27	18.4	4.2	20	1	US-09-073-465-16	Sequence 16, Appl
c	28	18.4	4.2	20	1	US-09-762-633-6	Sequence 6, Appli
c	29	18	4.1	19	1	US-09-998-551E-2	Sequence 2, Appli
c	30	17.4	3.9	19	1	US-07-971-819A-15	Sequence 15, Appl
c	31	17.4	3.9	19	1	US-08-384-490-29	Sequence 29, Appl
c	32	17.4	3.9	19	1	US-08-244-269-26	Sequence 26, Appl
c	33	17.4	3.9	19	1	US-08-475-231-15	Sequence 15, Appl
c	34	17.4	3.9	19	1	US-08-348-683-1	Sequence 1, Appli
c	35	17.4	3.9	19	1	US-08-459-383-29	Sequence 29, Appl
c	36	17.4	3.9	19	1	US-08-665-565B-2	Sequence 2, Appli
c	37	17.4	3.9	19	1	US-08-665-565B-4	Sequence 4, Appli
c	38	17.4	3.9	19	1	US-09-034-724-2	Sequence 2, Appli
c	39	17.4	3.9	19	1	US-09-034-724-4	Sequence 4, Appli
c	40	17.4	3.9	19	1	US-09-191-099-10	Sequence 10, Appl
c	41	17.4	3.9	19	1	US-09-216-909-5	Sequence 5, Appli
c	42	17.4	3.9	19	1	US-09-311-260-166	Sequence 166, App
c	43	17.4	3.9	19	1	US-09-702-843-5	Sequence 5, Appli
c	44	17.4	3.9	19	1	US-09-702-847-5	Sequence 5, Appli
c	45	17.4	3.9	19	1	US-08-943-571-4	Sequence 4, Appli
c	46	17.4	3.9	19	1	US-09-549-853-6	Sequence 6, Appli
c	47	17.4	3.9	19	1	US-09-437-905-2	Sequence 2, Appli
c	48	17.4	3.9	19	1	US-09-437-905-4	Sequence 4, Appli
c	49	17.4	3.9	19	1	US-09-848-083-2	Sequence 2, Appli
c	50	17.4	3.9	19	1	US-09-714-780-4	Sequence 4, Appli
c	51	17.4	3.9	19	1	US-09-687-219-2	Sequence 2, Appli
c	52	17.4	3.9	19	1	US-09-848-651-2	Sequence 2, Appli
c	53	17.4	3.9	19	1	US-09-848-095-2	Sequence 2, Appli
c	54	17.4	3.9	19	1	US-10-272-490-94	Sequence 94, Appl
c	55	17.4	3.9	19	1	US-10-053-243-8	Sequence 8, Appli
c	56	17.4	3.9	19	1	US-09-444-112-2	Sequence 2, Appli
c	57	17.4	3.9	19	1	US-10-214-473-83	Sequence 83, Appl
c	58	17.4	3.9	19	1	US-09-663-620-4	Sequence 4, Appli
c	59	17.2	3.9	23	1	US-09-335-231-4	Sequence 4, Appli
	60	17	3.8	17	1	US-08-144-212-18	Sequence 18, Appl
c	61	17	3.8	17	1	US-07-744-282C-118	Sequence 118, App
c	62	17	3.8	17	1	PCT-US92-06821A-124	Sequence 124, App
	63	17	3.8	22	1	US-08-412-614-101	Sequence 101, App
	64	17	3.8	22	1	US-08-412-614-103	Sequence 103, App
	65	17	3.8	22	1	US-08-635-761-101	Sequence 101, App
	66	17	3.8	22	1	US-08-635-761-103	Sequence 103, App
c	67	17	3.8	22	1	US-09-066-046-41	Sequence 41, Appl
	68	17	3.8	22	1	US-09-312-520-101	Sequence 101, App
	69	17	3.8	22	1	US-09-312-520-103	Sequence 103, App
	70	17	3.8	22	1	US-09-863-086-101	Sequence 101, App
	71	17	3.8	22	1	US-09-863-086-103	Sequence 103, App
c	72	17	3.8	23	1	US-08-778-217-8	Sequence 8, Appli
c	73	17	3.8	23	1	US-08-821-948-8	Sequence 8, Appli
	74	17	3.8	23	1	US-08-765-332-155	Sequence 155, App
	75	17	3.8	23	1	US-09-448-894-155	Sequence 155, App

c	76	17	3.8	23	1	US-09-397-955C-8	Sequence 8, Appli
	77	17	3.8	23	1	US-09-931-486-155	Sequence 155, App
	78	16.8	3.8	20	1	US-08-445-289B-8	Sequence 8, Appli
c	79	16.4	3.7	18	1	US-10-069-977-3	Sequence 3, Appli
c	80	16.4	3.7	18	1	US-09-786-253-9	Sequence 9, Appli
c	81	16.2	3.7	17	1	US-08-733-816-2	Sequence 2, Appli
c	82	16.2	3.7	17	1	US-08-892-540-2	Sequence 2, Appli
c	83	16.2	3.7	17	1	US-08-953-171-40	Sequence 40, Appl
c	84	16	3.6	16	1	US-09-342-579-3	Sequence 3, Appli
	85	16	3.6	16	1	US-09-398-179-17	Sequence 17, Appl
c	86	16	3.6	16	1	US-09-504-358-34	Sequence 34, Appl
c	87	16	3.6	16	1	US-09-617-854A-3	Sequence 3, Appli
c	88	16	3.6	16	1	US-09-954-314-34	Sequence 34, Appl
c	89	16	3.6	16	1	US-09-648-004-29	Sequence 29, Appl
c	90	16	3.6	16	1	US-09-716-865-25	Sequence 25, Appl
c	91	16	3.6	16	1	US-09-735-567-9	Sequence 9, Appli
c	92	16	3.6	16	1	US-10-230-562-34	Sequence 34, Appl
c	93	16	3.6	16	1	US-10-272-419-29	Sequence 29, Appl
c	94	16	3.6	16	1	US-10-007-527A-10	Sequence 10, Appl
c	95	16	3.6	16	1	US-09-941-947A-46	Sequence 46, Appl
c	96	16	3.6	16	1	US-10-209-372-24	Sequence 24, Appl
c	97	16	3.6	16	1	US-10-128-713A-22	Sequence 22, Appl
	98	16	3.6	17	1	US-08-242-664-34	Sequence 34, Appl
	99	16	3.6	17	1	US-08-484-138-34	Sequence 34, Appl
	100	16	3.6	17	1	US-09-052-333A-47	Sequence 47, Appl
	101	16	3.6	17	1	PCT-US95-06379-34	Sequence 34, Appl

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:26:20 ; Search time 1 Seconds  
(without alignments)  
3.446 Million cell updates/sec

Title: US-10-600-642A-2-COPY  
Perfect score: 442  
Sequence: 1 gaagtcgtaacaaggttagcc.....agcggttatggaaagttaa 442

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 142 seqs, 3898 residues

Total number of hits satisfying chosen parameters: 284

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 142 summaries

Database : ngssdb2:\*

Score / length  
Seq 2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	442	100.0	442	1	AAZ91772	Spacer region betw
2	442	100.0	442	1	AAI71856	Pectinatus frising
3	30.4	6.9	41	1	ADB61527	Prokaryotic gene s
4	29.8	6.7	40	1	AEC64592	Organochlorine com
5	26.8	6.1	30	1	ADX17032	Lemma minor chloro
c 6	26	5.9	26	1	AAQ92375	DNA primer. Synth
7	26	5.9	35	1	ACC97191	Consensus 16S rRNA
8	25	5.7	25	1	ADF69484	Tapesia acuformisI
c 9	23.8	5.4	27	1	AAX04478	Strain MO7 16S rDN
c 10	23.6	5.3	30	1	AAQ71864	Eucaryotic nuclear
11	23.6	5.3	30	1	AAI64203	Primer 1P for the
c 12	23.4	5.3	25	1	AAQ44665	Primer #1 for PCR/
c 13	22.2	5.0	27	1	AAV17792	Microorganism MO7
c 14	22	5.0	22	1	AAX04638	PCR primer 2 used
c 15	22	5.0	22	1	AAZ09417	E. coli 16S rRNA s
16	22	5.0	22	1	AAK99084	S. aureus 16S-rRNA
c 17	22	5.0	22	1	ABN84205	Salinospora sp. 16
18	22	5.0	22	1	AAK99123	Staphylococcus aur

c	19	22	5.0	22	1	ADS18913	Reverse PCR primer
c	20	22	5.0	22	1	ADU40707	Novel nucleotide a
c	21	22	5.0	22	1	ADZ66121	16s rRNA reverse P
c	22	22	5.0	22	1	ADU76905	16s rRNA reverse P
c	23	22	5.0	22	1	ADZ69178	Eubacterial PCR pr
c	24	22	5.0	22	1	AEC81382	Dehalococcoides ba
c	25	22	5.0	22	1	AEF24204	rRNA SSU primer RC
c	26	21.6	4.9	22	1	AAX82007	Bacterial 16S rRNA
c	27	21.6	4.9	22	1	AAZ86877	16S rRNA PCR prime
c	28	21.6	4.9	22	1	AAF54840	Primer used for sp
c	29	21.6	4.9	22	1	ABZ69287	J lividum 16s ribo
c	30	21.6	4.9	22	1	ABZ23953	A. radiobacter 16S
c	31	21.6	4.9	22	1	ADG25781	Bacterial universa
c	32	21.6	4.9	22	1	ADK65756	Reverse primer 149
c	33	21.6	4.9	22	1	ADU39844	Alcanivorax sp. OK
c	34	21.6	4.9	22	1	ADV25289	Primer 1492R used
c	35	21.6	4.9	22	1	ADW16281	PCR primer 1492r t
	36	21.4	4.8	23	1	ADS17007	Primer used to det
c	37	21.2	4.8	27	1	ADE85928	Escherichia coli 1
c	38	21	4.8	21	1	AAQ10127	Probe 1640 to the
c	39	21	4.8	21	1	AAT11573	16S rRNA reverse p
c	40	21	4.8	21	1	AAV21120	16S rRNA Escherich
	41	21	4.8	21	1	AAH73860	Cyanophycean PCR p
c	42	21	4.8	21	1	ACC48610	Erwinia pyrifoliae
c	43	21	4.8	21	1	ADL15738	Bacillus CMB26 str
c	44	21	4.8	21	1	ADS75285	Universal PCR prim
c	45	21	4.8	21	1	AEC09675	Primer 16S-2, seq
c	46	21	4.8	21	1	AEE19758	Pseudomonas chloro
c	47	21	4.8	21	1	AEE75252	Acinetobacter sp.
	48	21	4.8	24	1	AAI69778	16S/23SrRNA spacer
c	49	20.6	4.7	21	1	AAT60344	Reverse primer for
c	50	20.6	4.7	21	1	AAV45917	Biosensor oligonuc
c	51	20.6	4.7	21	1	AAX57749	Oligonucleotide 14
c	52	20.6	4.7	21	1	AAC58781	Bacterial 16S rRNA
c	53	20.6	4.7	21	1	ABS53672	Antimicrobial agen
c	54	20.6	4.7	21	1	ADV96672	Rhizobium 16S rDNA
	55	20.4	4.6	22	1	ABQ78789	PCR primer Eubl492
c	56	20.4	4.6	22	1	ADF17490	Pseudomonas putida
c	57	20.4	4.6	22	1	ADW16284	PCR primer 1492r t
c	58	20.4	4.6	22	1	AEC37152	H. variabilis 16S
c	59	20	4.5	20	1	AAQ54377	LAB rRNA gene prim
	60	20	4.5	20	1	AAQ65326	PCR primer R16-2 t
	61	20	4.5	20	1	AAQ62069	Lactobacillus 16S/
	62	20	4.5	20	1	AAQ88202	Lactobacillus sp.
	63	20	4.5	20	1	AAT45337	Mycoplasma second
	64	20	4.5	20	1	AAA08717	Bartonella genus s
c	65	20	4.5	20	1	AAA39039	Unknown bacterial
c	66	20	4.5	20	1	AAH73455	Brevibacillus bors
c	67	20	4.5	20	1	AAF95144	rrs gene PCR prime
c	68	20	4.5	20	1	AAH26928	Brevibacillus bors
c	69	20	4.5	20	1	ABQ75101	16S rDNA PCR prime
c	70	20	4.5	20	1	ACA99381	Enzyme DNA PCR pri
c	71	20	4.5	20	1	ADD29134	Nitrification bact
	72	20	4.5	20	1	ADK70934	Cff DNA related PC
c	73	20	4.5	20	1	ADF56681	Saccharothrix sp 1
c	74	20	4.5	20	1	ADG64526	PCR primer GMG 6 #
c	75	20	4.5	20	1	ADG64530	PCR primer GMG 9 #

c	76	20	4.5	20	1	ADQ78389	16S rRNA related p
c	77	20	4.5	20	1	ADQ67901	PCR primer BSR IS4
c	78	20	4.5	20	1	ADQ67897	PCR primer BSR IS4
c	79	20	4.5	20	1	ADQ74959	Sphingomonas sp. K
c	80	20	4.5	20	1	ADS15244	H.pylori 16s rRNA
c	81	20	4.5	20	1	ADS15215	Primer used in 16s
c	82	20	4.5	20	1	ADU39842	Acinetobacter sp.
c	83	20	4.5	20	1	ADW43199	Universal bacteria
c	84	20	4.5	20	1	ADY86154	16s rDNA amplifyin
c	85	20	4.5	20	1	ADY86158	16s rDNA amplifyin
c	86	20	4.5	20	1	ADZ99827	Primer used to amp
c	87	20	4.5	20	1	AED29539	Bacillus sp. 16S r
c	88	20	4.5	20	1	AED67223	Microbe WatG 16S r
c	89	20	4.5	20	1	AE97981	16S rDNA gene PCR
c	90	20	4.5	20	1	AE98064	16S rDNA gene PCR
c	91	20	4.5	22	1	ADS16972	16s and 18s rDNA g
	92	20	4.5	25	1	ADX82366	Lactobacillus forw
	93	19.8	4.5	23	1	AAA14177	M. pneumoniae 16S-
	94	19.8	4.5	26	1	AED69061	Kelp gametocyte rD
c	95	19.6	4.4	20	1	AAV34338	Burkholderia casid
c	96	19.6	4.4	20	1	AAX01434	Probe for Bacteroi
c	97	19.6	4.4	20	1	AAX59995	PCR primer 15R use
c	98	19.6	4.4	20	1	ABL59060	Nucleotide sequenc
c	99	19.6	4.4	20	1	ADM81035	Microbial 16SrDNA
c	100	19.6	4.4	20	1	AEA15813	Human Enterobacter
c	101	19.4	4.4	21	1	AAQ10128	Probe 1641 to the
c	102	19.4	4.4	21	1	AAQ10126	Probe 1639 to the
c	103	19.4	4.4	21	1	AAT11574	16S rRNA reverse p
c	104	19.4	4.4	21	1	AAT11572	16S rRNA reverse p
c	105	19.4	4.4	21	1	AAV21119	16S rRNA Escherich
c	106	19.4	4.4	21	1	AAV21121	16S rRNA Escherich
c	107	19.4	4.4	21	1	ADY97904	Bacillus subtilis
c	108	19.2	4.3	20	1	AAV61116	Lactobacillus sp.
c	109	19.2	4.3	20	1	AAV58223	Lactobacillus sp.
c	110	19.2	4.3	20	1	ADQ16363	PCR primer used to
c	111	19.2	4.3	20	1	AEA01079	Eubacterial 16S rD
	112	19.2	4.3	20	1	AEB93870	Mycoplasma PCR pri
c	113	19	4.3	19	1	AAZ91775	Spacer region betw
c	114	19	4.3	19	1	AAA92293	16S ribosomal DNA
c	115	19	4.3	19	1	AAF82059	16SrRNA PCR primer
c	116	19	4.3	19	1	AAF82062	16SrRNA PCR primer
c	117	19	4.3	19	1	AAI71859	Pectinatus frising
c	118	19	4.3	19	1	ABA04396	Fucophilus fucoida
c	119	19	4.3	19	1	ADF91902	16S ribosomal DNA
c	120	19	4.3	19	1	ADO42929	Primer of the inve
c	121	19	4.3	19	1	ADQ94518	Melanin inhibitor-
c	122	19	4.3	19	1	ADS19039	PCR primer used to
c	123	19	4.3	19	1	ADW11499	PCR primer used to
	124	19	4.3	19	1	ADW42907	Lactobacillus dete
	125	19	4.3	19	1	ADW42918	Lactobacillus dete
c	126	19	4.3	19	1	ADY71484	Geobacillus solubi
c	127	19	4.3	19	1	AEC08761	16s ribosomal DNA
	128	19	4.3	20	1	AAQ62086	Lactobacillus 16S/
	129	19	4.3	20	1	AAQ88220	Lactobacillus sp.
c	130	19	4.3	20	1	ADP47554	Intelligent PCR pr
c	131	19	4.3	20	1	ADQ59912	Intelligent PCR pr
c	132	19	4.3	20	1	AEC39825	D-hydantoinase enz

c 133	19	4.3	20	1	AED28920	Primer for PCR det
c 134	19	4.3	20	1	AEF81510	Halorubrum sp. BD-
c 135	19	4.3	20	1	AEE18738	Eubacteria univers
c 136	19	4.3	20	1	AEE94389	Universal bacteria
c 137	19	4.3	21	1	AAA74501	PCR primer ENV2B.
c 138	19	4.3	21	1	ABK14158	Chlorinated ethyle
c 139	19	4.3	21	1	ADN59207	Microorganism moni
c 140	19	4.3	21	1	ADN96852	Bacterial 16S rDNA
c 141	19	4.3	21	1	AEC07076	16S rRNA PCR prime
142	19	4.3	23	1	AEA61056	Mycobacterium prob



OM nucleic - nucleic search, using sw model

Run on: August 18, 2006, 15:28:49 ; Search time 0.001 Seconds  
 (without alignments)  
 675.376 Million cell updates/sec

Title: US-10-600-642A-2-COPY  
 Perfect score: 442  
 Sequence: 1 gaagtcgtaacaaggttagcc.....agcggttatggaaagttaa 442

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 0.5

Searched: 33 seqs, 764 residues

Total number of hits satisfying chosen parameters: 66

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 33 summaries

Database : pubnewdb2:\*

*score/length PG Pub new 8102*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	5.7	25	1	US-11-348-413-605683	Sequence 605683,
2	25	5.7	25	1	US-11-348-413-988264	Sequence 988264,
c 3	22	5.0	28	1	US-11-401-826-7	Sequence 7, Appli
c 4	22	5.0	28	1	US-11-255-290-7	Sequence 7, Appli
c 5	21.6	4.9	22	1	US-11-265-833-2	Sequence 2, Appli
c 6	21.2	4.8	27	1	US-11-368-333-6	Sequence 6, Appli
c 7	20	4.5	20	1	US-10-510-329-13	Sequence 13, Appli
c 8	20	4.5	20	1	US-11-324-675-2	Sequence 2, Appli
c 9	19	4.3	19	1	US-11-373-989-2	Sequence 2, Appli
10	18.8	4.3	25	1	US-11-348-413-1009479	Sequence 1009479,
11	18.6	4.2	25	1	US-11-348-413-1064914	Sequence 1064914,
c 12	18.6	4.2	25	1	US-11-348-413-1165354	Sequence 1165354,
13	18.6	4.2	25	1	US-11-348-413-1210461	Sequence 1210461,
14	18.6	4.2	25	1	US-11-348-413-1210462	Sequence 1210462,
c 15	18.2	4.1	25	1	US-11-348-413-202363	Sequence 202363,
16	18.2	4.1	25	1	US-11-348-413-1055941	Sequence 1055941,
c 17	18	4.1	18	1	US-11-350-955-9	Sequence 9, Appli
c 18	18	4.1	18	1	US-11-350-796-9	Sequence 9, Appli

C	19	17.8	4.0	25	1	US-11-348-413-1009551	Sequence 1009551,
C	20	17.6	4.0	25	1	US-11-348-413-222739	Sequence 222739,
	21	17.6	4.0	25	1	US-11-348-413-434686	Sequence 434686,
	22	17.6	4.0	25	1	US-11-348-413-434687	Sequence 434687,
	23	17.6	4.0	25	1	US-11-348-413-572608	Sequence 572608,
C	24	17.6	4.0	25	1	US-11-348-413-900967	Sequence 900967,
	25	17.6	4.0	25	1	US-11-348-413-930121	Sequence 930121,
	26	17.6	4.0	25	1	US-11-348-413-1075989	Sequence 1075989,
	27	17.6	4.0	25	1	US-11-348-413-1238534	Sequence 1238534,
C	28	17.4	3.9	19	1	US-10-034-622-2	Sequence 2, Appli
C	29	17.4	3.9	19	1	US-11-134-852-2	Sequence 2, Appli
C	30	17.4	3.9	19	1	US-11-235-479-5	Sequence 5, Appli
C	31	17	3.8	17	1	US-10-524-152A-12	Sequence 12, Appl
C	32	17	3.8	18	1	US-10-524-152A-10	Sequence 10, Appl
	33	16.4	3.7	22	1	US-10-535-629-9	Sequence 9, Appli